

8072

GAACAGATTTGGAATAACATGACCTGGA TGGAGTGGGACAGAGAAATTAA

GAAGAGATTTGGGAGAACATGACCTGGATGCAGTGGGAAAAGAAATTCA

GAAACAATTTGGGATAACATGACCTGGATCCACTGGGAAAGAGAAATTGA

GAAACAATTTGGGATAACATGACCTGGATGCAGTGGGAAAGAGAAATTGA

GAAATTAA

8121

CAATTACACAAGCTTAATACACTCCTTAATTGAAGAATCGCAAACCAGC

CAATCACACAAAATACATATACTCCTTACTTGAAAATCGCAGAACCAAC

CAATTACACAAACATAATATACACCTTAATTGAAGAATCGCAGAACCAAC

CAATTACACAAACATAATATACACCTTAATTGAAGAATCGCAGAACCAAC

CAATTACACAAGATTAATATACAACCTTAATTGAAGAATCGCAGAACCAAC

8171

FIGURE 1

00146783-000398

AAGAAAAGAATGAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTTG

AAGAAAAGAATGAACAAGAACTATTGGAATTGGATCAATGGGCAAGTTTG

AAGAAAAAATGAAC TAGAATTATTGGAATTGGATAAATGGGCAAATTTG

AACAAAAAATGAAC TAGAATTATTGGAATTGGATAAATGGGCAAATTTG

AAGAAAAGAATGAACAAGACTTATTGGAATTAGATAAATGGGCAAGTTTG

8221

TGGAATTGGTTTAACATAACAAATTGGCTGTGGTATATAAAATTATTCAT

TGGAATTGGTTTGACATAACAAATGGCTGTGGTATATAAAATATTCAT

TGGAATTGGTTTAGTATATCAAACTGGCTATGGTATATAAAATTATTCAT

TGGAATTGGTTTAGTATATCAAACTGGCTATGGTATATAAAATTATTCAT

TGGAATTGGTTTGACATAACAAGTGGGCTGTGGTATATAAAATTATTCAT

8271

FIGURE 1

0914633-090399

AATGATAGTAGGAGGCTTGGTAGGTTAAGAATAGTTTTTGCTGTACTTT
 * * * * *
 AATGGTAGTAGGAGGCTTGGTAGGTTAAGAATAGTTTTTGCTGTACTTT
 * * * * *
 AATGGTAGTAGGAGGCTTGGTAGGTTAAGAATAGTTTTTACTGTACTTT
 * * * * *
 AATGGTAGTAGGAGGCTTGGTAGGTTAAGAATAGTTTTTACTGTACTTT
 * * * * *
 AATGATAGTAGGAGGCTTGGTAGGTTAAGAATAGTTTTAGCTGTACTTT

8321

SA8 SA9

SA10

CTATAGTGAATAGAGTTAGGCAGGGATACTCACCATTATCGTTTCAGACC
 * * * * *
 CTATAGTGAATAGAGTTAGGCAGGGATACTCACCATTATCGTTTCAGACC
 * * * * *
 CTATAGTGAATAGAGTTAGGCAGGGATACTCACCATTATCGTTTCAGACC
 * * * * *
 CTATAGTGAATAGAGTTAGGCAGGGATACTCACCATTATCGTTTCAGACC
 * * * * *
 CTATAGTGAATAGAGTTAGGCAGGGATACTCACCATTATCGTTTCAGACC

8371

FIGURE 1

09145703 000398

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Tat terminati n NL43

CACCTCCCAATCCCGAGGGGACCCGACAGGCCCGAAGGAATAGAAGAAGA 8421
*** **
CTCCTCCCAACCCCGAGGGGACCCGACAGGCCCGAAGGAATCGAAGAAGA

CACCTCCCAACCCCGAAGGGACCCGACAGGCCAGAAGGAATCGAAGAAGA

CACCTCCCAACCCCGAGGGGACCCGACAGGCCAGAAGGAATCGAAGAAGA

CACCTCCCAACCCCGAGGGGACCCGACAGGCCCGAAGGAATCGAAGAAGA

AGGTGGAGAGAGAGACAGAGACAGATCCATTGATTAGTGAACGGATCCT 8471

AGGTGGAGAGAGAGACAGAGACAGATCCACTCCATTAGTACACGGATTCT

AGGTGGAGAGAGAGACAGAGGCAGCTCCACTCGATTAGTGCACGGATTCT

AGGTGGAGAGAGAGAGGCAGAGGCAGTCCACTCGATTAGTGCACGGATTCT

AGGTGGAGAGAGAGACAGAGACAGATCCAGTCGATTAGTGCACGGATTCT
D36P, C18S, C18M & C98H Tat termination

FIGURE 1

TAGCACTTATCTGGGACGATCTGCGGAGCCTGTGCCTCTTCAGCTACCAC

TAGCACTTTTCTGGGACGACCTGAGGAGCCTGTGCCTCTTCCTCTACCAC

TAGCACTTTTCTGGGACGACCTGAGGAGTCTGTGCCTCTTCAGCTACCAC

TAGCACTTTTCTGGGTGACCTGAGGAGTCTGTGCCTCTTCAGCTACCAC

TAGCACTTTTCTGGGTGACCTGAGGAGCCTGTGCCTCTTCAGCTACCAC

8521

CGCTTGAGAGACTTACTCTTGATTGTAACGAGGATTGTGGA ACTTCTGGG
*
CACTTGAGAGACTTACTCTTGATTGTAACAAGGATTGTGGA ACTTCTGGG
*
CACTTGAGAGACTTACTCTTGATTGTAACGAGGATTGTGGA ACTTCTGGG
*
CGCTTGAGAGACTTACTCTTGATTGTAACGAGGATTGTGGA ACTTCTGGG
*
CGCTTGAGAGACTTACTCTTGATTGTAACGAGGATTGTGGA ACTTCTGGG

8571

FIGURE 1

6/101



ACGCAGGGGGTGGGAAGCCCTCAAATATTGGTGGAATCTCCTACAGTATT
** ***** **
ACGCAGGGGGATGGGAAGCCCTCAAATATTGGTGGAACCTCCTAAAGTATT
**** **
ACGCAGGGGGATGGGAAGCCCTCAAATACTGGTGGAATCTCCTGCAGTATT

ACGCGGGGGATGGGAAGCCCTCAAATACTGGTGGAATCTCCTGCAGTATT

ACGCAGGGGGTGGGAAGCCCTCAAATATTGGTGGAATCTCCTACAATATT

8621

NL43 Rev termination

GGAGTCAGGAACTAAAGAAATAGTGCTGTTAACTTGCTCAATGCCACAGCC

GGAGCCAGGAACTGCAGAAGAGTGCTGTTATCTTCCTCAATGCCACCGCC

GGAGGCAGGAACTACAGAAGAGTGCTGTTAGCTTGTTCAATGGCACGGCC

GGAGACAGGAACTACAGAAGAGTGCAAGTTAGCTTGTTCAATGCCATAGCC

GGAGTCAGGAACTCAAGAAGAGTGCTATTAGCTTGTTCAATGCCACCGCC

8671

C18S, C18M & C98H Rev termination

FIGURE 1

09146783 090398
06E060 E324T60

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ATAGCAGTAGCTGAGGGGACAGATAGGGTTATAGAAGTATTACAAGCAGC
* * * * *

8721

ATAGCAGTAGCTGAGGGGACAGATAGAGTTTATAGAAGTATTACAAGAGC
* * * * *

ATAGCAGTAGCTGAGGGGACAGATAGAGTTATAGAAGCTTTACCAAGGGC
* * * * *

ATAGCAGTAGCTGAGGGGACAGATAGAGCTATAGAAGGATTACAAACACC
* * * * *

ATAGCAGTAGCTGAGGGGACAGATAGAGTTATAGAAGTATTACAAGAGC
* * * * *

incomplete . AGGGGACAGATAGAGTTCTAGAAGTATTACAAGAGC
D36P Rev termination

TTATAGAGCTATTCGCCACATACCTAGAAGAATAAGACAGGGGCTTGGAAA
* * * * *

8771

TTATAGAGCTATCCTCCACATACCTAGAAGAATAAGACAGGGCCTCGAAA
* * * * *

TTATAGAGCTATTCCTCCACATACCTAGAAGAATAAGACAGGGGCTTAGAAA
* * * * *

TTATAGAGCTATTCCTCCACATACCTAGAAGAATAAGACAGGGGCTTAGAAA
* * * * *

TTGTAGAGCTGTTCTCCACATACCTAGAAGAATAAGACAGGGGCTTCGAAA
* * * * *

TTATAGAGCCATTCTCCACATACCTAGAAGAATAAGACAGGGGCTTCGAAA

FIGURE 1

00146788 090399

FIGURE 1

9/101

GGGTGGGAGCAGTATCTCGAGACCTAGAAAAACATGGAGCAATCACAAGT
* * * * *

8921

GGGTGGGGGC-----

GGGTGGGAGCAATATCTCGAGACCTAGGAAAACATGGAGCAATCCCAAGT

GGGTGGGAGC-----

SIV_{mac239} IPTC

AGCAATACAGCAGCTAACAATGCTGCTTGTGCCTGGCTAGAAGCACAAGA
* * * * *

8971

-----CAACAACTAACAATGCTGATCGTGCCTGGCTAGAAGCACAAGA

AGCAATACAACAACTAACAATGCTAATTGTGCCTGGCTAGAAGCACAAGA
* * * * *

-----CAACAACTAACAATTCTGGTTGCGCCTGGCTAGAAGCA-----

FIGURE 1

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GGAGGAAGAGGTGGGTTTTCCAGTCACACCTCAGGTACCTTTAAGACCAA

9021

GAAGGAAGAAGCGGGTTTTCCAGTCAAACCTCAGGTA-----

-----TACCTTTAAGAC--

GGAGGAGGAAGTGGGTTTTCCAGTCAAACCTCAGGTACCTTTAAGACCAA

Poly purine tract

TGACTTACAAGGCAGCTGTAGATCTTAGCCACTTTTTTAAAGAAAAGGGG

9071

-----GCTGTAGATCTTAGCCACTTTTTTAAAGAAAAGGGG

-----AAGGCAGCTATAGATCTTAGCCGCTTTTTTAAAGAAAAGGGG

-----GATCTTAGCCACTTTTTTAAAGAAAAGGGG

TGACTTACAAG-----GCCACTTTTTTAAAGAAAAGGGG

-----CACTTTTTTAAAGAAAAGGGG

C18S nef termination

C18M and C98H nef Termination

FIGURE 1

11/101

[U3

GGACTGGAAGGGCTAATTCACCTCCCAAAGAAGACAAGATATCCTTGATCT

9121

GGACTGGAAGGGCTAATTCACCTCCCAAAGAAGACAAGATA-----

GGACTGGAAGGGCTAATTCACCTCACAGAGAAGA-----

GGACTGGAAGGGCTAATTCACCTCACAGAGAAGA-----

GGACTGGAAGGGCTAATTCACCTCCTAAAGAAGACAAGATATCCTTGATCT

GGACTGGAAGGGCTAATACGCTCCCAAAGAAGACAAGATATCCTTGATCT

SA12

GTGGATCTACCACACACAAGGCTACTTCCCTGATTGGCAGAACTACACAC

9171

TTGGATCTACCACACACAAGGCTACT-----

**** *****

GTGGGGCTACCACACACAAGGCTACTTCCCTGATTGGCAGAACGACACAC

FIGURE 1

09145703 090900Z

12/101



{...dyad symmetry...
{...NRT-1.....

{ NRE -->

CAGGGCCAGGGGTCAGATATCCACTGACCTTTGGATGGTGCTACAAGCTA

9221

-----CACAGTGCTGCAAACCTA

-----ATCCACTGACTTTTGG, TGGTGCTTCAAATTA

CAGGGCCAGGGACCAGATATCCACTGACCTTTGGATGGTGCTGCAAACGA

.....)

.....)

myb

NF-AT

GTACCAGTTGAGCCAGAT AAGGTAGAAGAGGCCAATAAAGGAGAGAACAC

9271

TACCAGTGGAGTCAGCGAAGATAGAAGAGGCCAATGGAGGAGAAAACCA

---TCAGTTGAACCAGAAGAAGATAGAAGAGGCCATGAAGAAGAAAACAA

---TCAGTTGAACCAGAAGAAGATGAAGAGGCCATGAAGAAGAAAACAA

GTACCAGTGGANCCAGA--AGAGAGAAGAGACCAATGGAGGAGAGAACA-

GTACCAGGGGAAACAGAGAAGATAGAAGAGGCCAATGGAGGAGAAAACAA

(myb)

FIGURE 1

13/101

NF-AT

CAGCTTGTTACACCCTGTGAGCCTGCATGGAATGGATGACCCTGAGAGAG
*** **

9321

CAGATTGTT-----
*** **

CAGATTGTT-----
*** **

CAGATTGTT-----

*** **

CAGACTGTT-----

USF

<-- NRE]

AAGTGTTAGAGTGGAGGTTTGACAGCCGCCTAGCATTTCATCACGTGGCC

9371

* * *
-----CCGTTTGTT

* *
-----CTGCT

-----A

FIGURE 1

14/101

TCF-1a

N f terminati n

CGAGAGCTGCATCCGGAGTACTTCAAGAACTGCTGACATCGAGCTTGCTA 9421
 * * * * *
 CTGTTGGGGACTTTCCATCCGTTGGGGACTTTCCAAGGCGGCGTGCCCTG
 * * * * *
 CCGTTGGGGACTTTCCA, , , , , GGAGACGTGGCCTGAGTGATAAGCCG
 * * * * *
 TGCTCAGCTGGGGACTTTCCAGAAGGCGCGGCCTGAGTGACTAAGCCCCG
 * * * * *
 CAGAGTGTGGGGACTCTCCACAACAGAGTGTGGGGACTTTCCAAGGAGGC
 * * * * *
 ----CCGTTGGGGACTTTCCAAGGAGGCGTGCCCTGAGTGACTAAGTTCC
 D36P, C18S, C18M & C98H extra NFkB
 D36P & C98H extra NFkB

NFkB	NFkB	Sp1	
CAAGGGACTTTCCG, , , , ,	CTGGGGACTTTCCAG, GGAGGCGTGGC		9461
* * * * *	* * * * *	* * * * *	
GGTGACTAGTTCCG, , , , ,	GTGGGGACTTTCCAA, GAAGGCGCGGC		
* * * * *	* * * * *	* * * * *	
CTGGGGACTTTCCGAAGAGGCGTGACGGGACTTTCCAA, GGCGACGTGGC			
* * * * *	* * * * *	* * * * *	
TTGGGACTTTCCGAAGAGGCATGAAGGGACTTTCCAAG, GCAGGCGTGGC			
* * * * *	* * * * *	* * * * *	
GTGGCCTGAGTGACTAAGTTCCGTTGGGGACTTTCCAA, AAAGGCGAGGC			
* * * * *	* * * * *	* * * * *	
GTTGGGACTTTCCAAGGAGGC, , GCGGGGACTTTCCAA, GGAGGCGCGGC			
C18S & C18M NFkB	NFkB	Sp1	
D36P and C98H 3'-half NFkB			

FIGURE 1

15/101

Sp1

Sp1

TATA box

CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG
 * * * * *
 CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG
 * * * * *
 CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG
 * * * * *
 CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG
 * * * * *
 CTGGGCGGA-CTGGGGAGTGC-GAGCC-, TCAGATGCTGCATATAGGCAG
 * * * * *
 CTGGGCGGGACTGGGGAGGGGCGAGCCC, TCAGATGCTGCATATAAGCAG

9510

Sp1

Sp1

U3

R

TAR

CTGCTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG
 * * * * *
 CTGCTTTCTGCTGTTACTGGGTCTCTCGGGTTAGACCAGATCTGAGCCTG
 * * * * *
 CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG
 * * * * *
 CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG
 * * * * *
 CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG
 * * * * *
 CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG
 * * * * *

9560

CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCT...incomplete

FIGURE 1

09146783 00398

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	Sp1	Sp1	TATA b x	
NL43	CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG			9510
D36P	CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG			
C18S	CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG			
C18M	CTGGGCGGGACTGGGGAGTGGCGAGCCC, TCAGATGCTGCATATAAGCAG			
C98H	CTGGGCGGA-CTGGGGAGTGC-GAGCC-, TCAGATGCTGCATATAGGCAG			
C54H2	CTGGGCGGGACTGGGGAGGGGCGAGCCC, TCAGATGCTGCATATAAGCAG			
	Sp1	Sp1		

	U3	R	TAR	
NL43	CTGCTTTTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG			9560
D36P	CTGCTTTCTGCTGTTACTGGGTCTCTCGGGTTAGACCAGATCTGAGCCTG			
C18S	CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG			
C18M	CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG			
C98H	CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTG			
C54H2	CTGCTTTCTGCCTGTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCT...incomplete			

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AACTAGAGATCCCTCAGACCCTTTTAGTCAGTGTGGAAAATCTCTAGCA 9709

* *****

ATCTAGA 1305

* *****

ATCTAGA 1209

* *****

ATCTAGAGATCCCTCAGACCATTTTAGTCCGTGTGGAAAATCTCTAGCA END

* *****

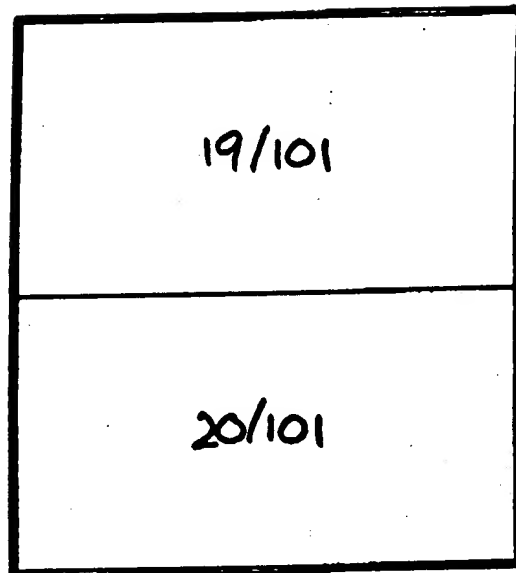
ATCTAGA 1399

FIGURE 1

00446783-100398

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FIGURE 2



86E060* EBZSH160

19/101

FIGURE 2A

86

PTSQSRGDP TGPKE#

NL43 73

PSSQPRGDP TGPKEKKKVERETETDPLD#

D36P BMC

PTSQPRRDPTGQESKKKVERETEAAPLD#

C18 HIV_{sev}

PTSQPRRDPTGQESKKKVERETEAAPLD#

C18 HIV_{MBC}

PTSQPRRDPTGQESKKKVERETETDPVD#

C98 HIV

FIGURE 2B

65

DPPPNEGTRQARRNRRRRWRERQRQIHSISERILSTYLG

NL43 26

DPPPNEGTRQARRNRRRRWRERQRQIHSISTRILSTFLG

D36P BMC

DPPPNEGTRQARRNRRRRWRERQRQLHSISARILSTFLG

C18 HIV_{stv}

DPPPNEGTRQARRNRRRRWRERQRQLHSISARILSTFLG

C18 HIV_{MBC}

DPPPNEGTRQARRNRRRRWRERQRQIQISARILSTFLG

C98 HIV

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FIGURE 2B

NL43 RSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVE 105

D36 PBMC RPEEPVPLPLPPLERLTLDNCNEDCGTSGTGGMGSPQILVE

C18 HIV_{stv} RPEESVPLQLPPLERLTLDNCNEDCGTSGTGGMGSPQILVE

C18 HIV_{mbc} RPEESVPLQLPPLERLTLDNCNEDCGTSGTGGMGSPQILVE

C98 HIV RPEEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVE

NL43 SPTVLESGTKE#

D36PBMC PPKVLEPGTAEECCYLAQCHRHSSS#

C18 HIV_{stv} SPAVLEAGTTECC#

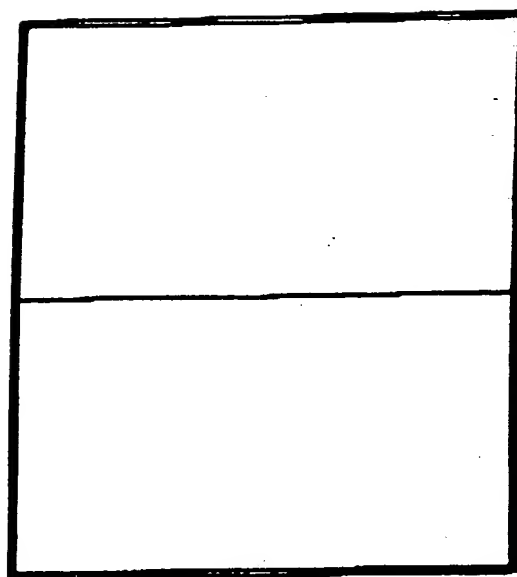
C18 HIV_{mbc} SPAVLEAGTTECC#

C98 HIV SPTILESGTQECCY#

116

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FIGURE 3



00146783-003398
000000-000000

FIGURE 3

611 NL43 EQIWNNTMENDREINNNTSLIHSLEESQSQKNEQELLELDKWASL 639
 612 D36P BMC BEIWENMTMQWEKEIHNTKYIYSLLEKSQSQKNEQELLELDQWASL
 613 C18 HIV_{StV} ETIWDNMTMQWEREIDNYTNIITYLLEESQSQKNELELELDKWANL
 C18 HIV_{MBC}
 C98 HIV EINNYTRTIYNLEESQSQKNEQDLELDKWASL

2/101

689 NL43 WNWENITNWLWYIKLFIMVGGVLGLRIVFAVLSIVNRVRQGYSPLSFQT
 D36 BMC WNWFDITKWLWYIKLFIMVGGVLGLRIVFAVLSIVNRVRQGYSPLSFQT
 C18 HIV_{StV} WNWFSISNWLWYIKLFIMVGGVLGLRIVFTVLSIVNRVRQGYSPLSFQT
 C18 HIV_{MBC}
 C98 HIV WNWFDITSGWLWYIKLFIMVGGVLGLRIVLAVLSIVNRVRQGYSPLSFQT

FIGURE 3

NL43 HLP1PRGPDPRPEGIEEGGERDRDRSIRLVNGSLALINDDLRSLCLFSYH 739

D36 PBMC LLPTPRGPDPRPEGIEEGGERDRDRSTRLVHGFLALFWDDLRLSLCLFLYH

C18 HIV_{STV} HLTPKGPDRPEGIEEGGERDRGSSTRLVHGFLALFWDDLRLSLCLFSYH

C18 HIV_{MC}

C98 HIV HLPTPRGPDPRPEGIEEGGERDRDRSSRLVHGFLALFWVDLRSLCLFSYH

NL43 RLRDLLLLIVTRIVELLGRRGWEALKYWNLLQYWSQELKNSAVNLLNATA 789

D36 PBMC HLRDLLLLIVTRIVELLGRRGWEALKYWNLLKYWSQELQKSAVILLNATA

C18 HIV_{STV} HLRDLLLLIVTRIVELLGRRGWEALKYWNLLQYWRQELQKSAVSLFNGTA

C18 HIV_{MC}

C98 HIV RLRDLLLLIVTRIVELLGRRGWEALKYWNLLQYWSQELKKSAISLFNATA

NL43 IAVAEGTDRVIEVLQAAAYRAIRHIPRIRROGLERILL# 839

D36 PBMC IAVAEGTDRVIEVLQRAYRAIRHIPRIRROGLEMALL#

C18 HIV_{STV} IAVAEGTDRVIEALRRAYRAIRHIPRIRROGLERALL#

C18 HIV_{MC}

C98 HIV IAVAEGTDRVIEVLQACRAVLHIPRIRROGFERAML#

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FIGURE 4

NL43	MGGKWSKSSVIGWPAVRRMRRAEPAADGVGAVSRDLEKHGAITSNTAA ***	50
D36 PBMC	MGGK# *****	4
C18.HIV _{Stv}	MGGKWSKSSVRRHVPLRQGSYRS# *	24
C18 HIV _{WBC}	MRILATF# *****	7
C98 HIV	MGGKWLKSSMVRWPAVREKMKQAEPAABGVGALSRLGKHGAIPSSNTTT	50
NL43	NNAACAWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGLEGL ***	100
C98 HIV	NNANCANLEAQEEEEVGFPVKPQVPLRPMTYKATF#	85
NL43	IHSQRRQDILDLIWYHTQGYFPDQNYTPGPGVRYPLTFGWCYKLVPEP	150
NL43	DKVEANKGENTSLHPVSLHGMDPPEREVLEWRFDLSLAFHHVARELHP	200
NL43	BYFKNC*	206

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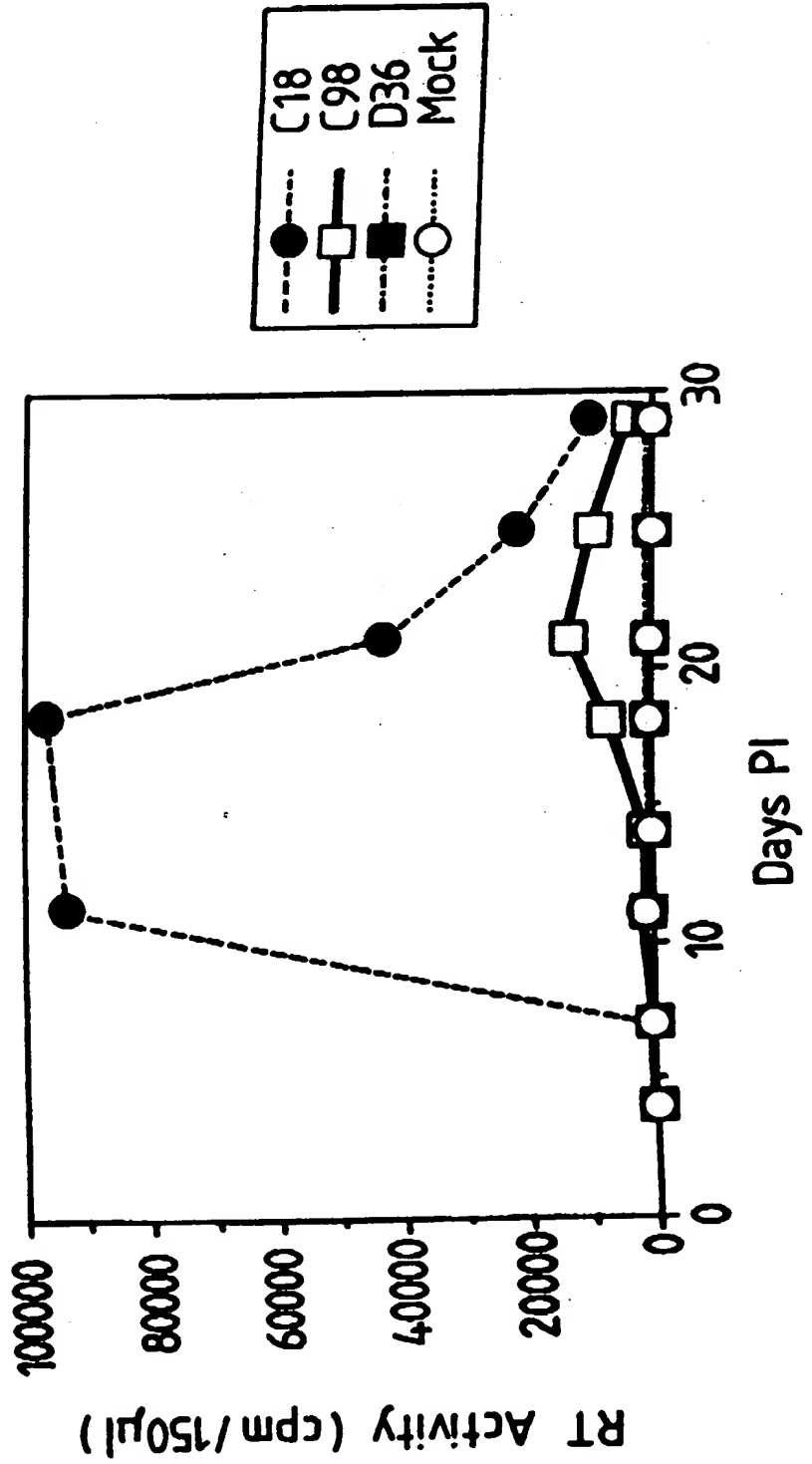
FIGURE 5

	NFkB	NFkB
9419 NL43	CGAGCTTGCTACAAGGGACTTTCC, , , , GCTGGGGACTTTCCAGGGA	
D36 PBMC	ACTGTTGGGGACTTTCCATCCGTTGGGGACTTTCCAGGC	
C18 HIV _{stc}	ACCGTTTGTTCCGTTGGGGACTTTCCA-GGA	
C18 HIV _{mbc}	ACTGCTTGCTCAGCTGGGGACTTTCCA-GAA	
C98 HIV	ΔACAGAGTGTGGGACTCTCCACACAGAGTGTGGGGACTTTCCAGGA	
C54 PBMC	ΔCCGTTGGGGACTTTCCAGGA	
	NFkB	NFkB
	Sp1	Sp1
NL43	GGCGTGGCCTGGGGGACTGGGGAGTGGCG-AGCCCTCA	9492
DC36 PBMC	GGCGTGGCCTGGGTGACTAGTTCGGTGGG-ACTTTCCA	
C18 HIV _{stc}	GACGTGGCCTGAGTGACTAAG-CGGCTGGG-ACTTTCCG	
C18 HIV _{mbc}	GGCGGGCCTGAGTGACTAAGCCCGTTGGG-ACTTTCCG	
C98 HIV	GGCGTGGCCTGAGTGACTAAGTTCGGTGGGACTTTCCA	
C54 PBMC	GGCGTGGCCTGAGTGACTAAGTTCGGTGGGACTTTCCAA	
	Sp1	3' half NFkB NFkB

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FIG 6

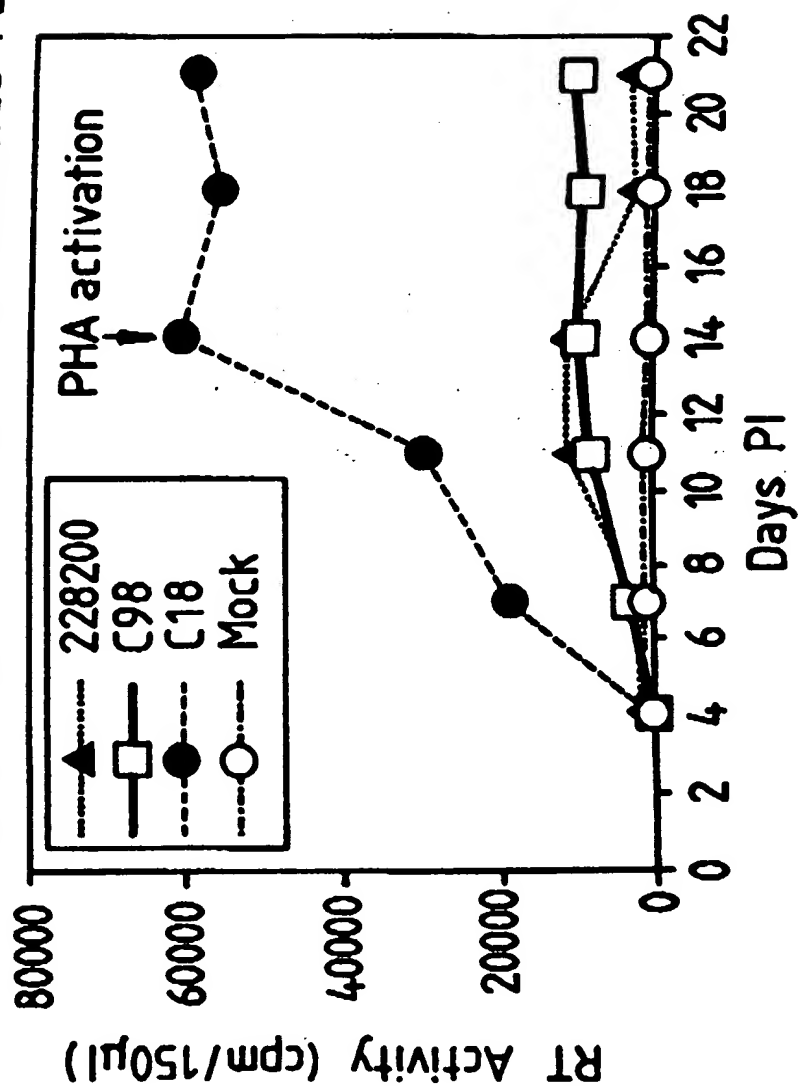
**Replication of Sydney Asymptomatic
Patients Isolates in PHA-stimulated PBMCs**



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FIG 7

Replication of Sydney Asymptomatic
Patient Isolates in non-PHA stimulated PBMCs



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FIG 8

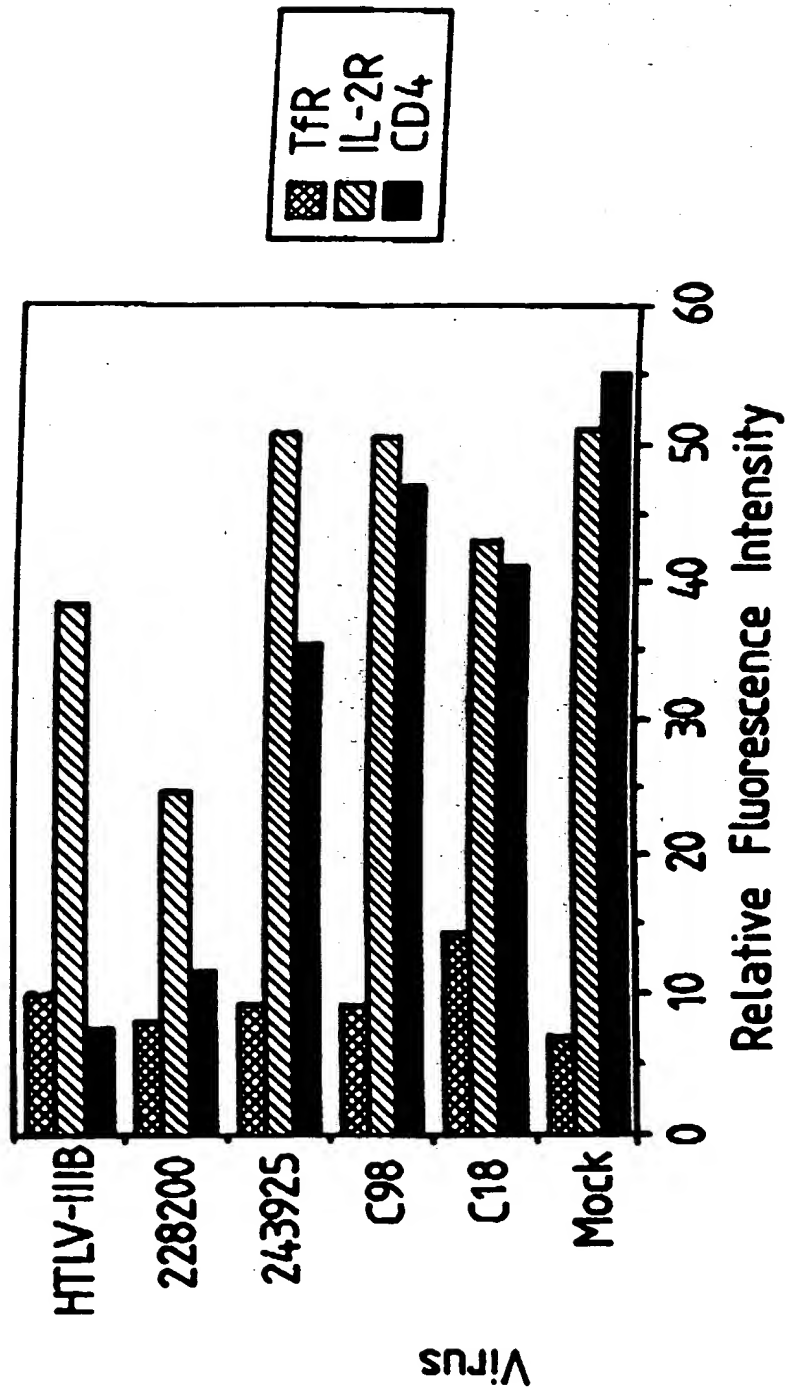


FIGURE 9

0314593-001300

FOR THE RECORD

TGGAAGGGCTAATTCACCTCACGGAAGACCAAGTTGAACCAAG
AAGAAGATAGAAGAGGCCATGAAGAAGAAAACAACAGATTGT
TCTGCTTGCTCAGCTGGGGACTTTCCAGAAGGCGCGGCCTGA
GTGACTAAGCCCCGTTGGGGACTTTCCGAAGAGGCATGAAGG
GACTTTCCAAGGCAGGCGTGGCCTGGGCGGGACTGGGGAGTG
GCGAGCCCTCAGATGCTGCATATAAGCAGCTGCTTTCTGCCT
GTACTGGGTCTCTCTGGTTAGACCAGATCTGAGCCTGGGAGC
TCTCTGGCTAGCTAGGGAACCCACTGCTTAAGCCTCAATAAA
GCTTGCCCTTGAGTGCTTCAAGTAGTGTGTGCCCGTCTGTTGT
GTGACTCTGGTATCTAGAGATCCCTCAGACCATTTTAGTCCG
TGTGGAAAATCTCTAGCAGTGGCGCCCCGAACAGGGACTTGAA
AGCGAAAGGAAAACAGAGGAGCTCTCTCGACGCAGGACTCG
GCTTGCTGAAGCGCGCACGGCAAGAGGCGAGGGGCGGCGACT
GGTGAGTACGCCGAAAATTTTGACTAGCGGAGGCTAGAAGGA
GAGAGATGGGTGCGAGAGCGTCAATATTAAGCGGGGGAAAAT
TAGATAGATGGGAGAAAATTCGGTTAAGGCCAGGAGGAAAGA
AAAAGTATAAATTA AAAACATATAGTATGGGCAAGCAGGGAGC
TAGAACGATTTCGCAGTCAATCCTGGCCTGTTGGAAACATCAG
AAGGCTGTAGACAAATACTGGGACAGTTACACCCGTCCCTTC
AGACAGGATCAGAAGAACTTAAATCAGTATATAATGCAGTAG
CAGTCCTCTATTGTGTGCATCAAAACATAGACATAAAGGACA
CCAAGGAAGCTTTAGAAAAGATAGAGGAAGAGCAAAACAAAT
GTAAGAAAAAAGCACAGCAAGCAGCAGCACAGCAAGCAGCAG
CTGGCACAGGAAACAGCAACCCGGTCAGCCAAAATTACCCTA
TAGTACAGAACATGCAGGGGCAAATGGTACATCAGGCCATAT
CACCTAGAACTTTAAATGCATGGGTAAAAGTAATAGAAGAGA
AGGCTTTTCAGCCCAGAGGTAATACCCATGTTTTTCAGCATTAT
CAGAAGGAGCCACCCCAAGATTTAACACCCATGCTAAACA
CAGTGGGGGGACATCAAGCAGCTATGCAAATGTTAAAAGAGA
CCATCAATGAGGAAGCTGCAGAATGGGATAGATTACATCCAG
CGCAGGCAGGGCCTGTTGCACCAGGCCAGATGAGAGACCCAA
GGGGAAGTGACATAGCAGGAACTACTAGTACCCTTCAGGAAC
AAATAGGATGGATGACAGGTAATCCAGCTATCCCAGTAGGAG
AAATCTATAAAAGATGGATAATCCTGGGATTAAATAAAATAG
TAAGGATGTATAGCCCTATCAGCATTCTGGACATAAAACAAG
GACCAAAGGAACCCCTTTAGAGACTATGTAGACCGGTTCTATA
AACTCTAAGAGCCGAGCAAGCTACACAGGAGGTAAAAAATT
GGATGACAGAAACCTTGTTGGTCCAAAATGCAAACCCAGATT
GTAAGACTATTTTAAAAGCATTGGGACCAGCAGCTACACTAG

AAGAAATGATGACAGCATGTCAGGGAGTGGGAGGACCCAGCC
ATAAAGCAAGAGTTTTTGGCAGAAGCAATGAGCCAAGCAACAA
ATGCAGCTACTGTAATGATGCAGAGAAGCAATTTTAGAAACC
AAAGAAAGAATGTTAAGTGTTTCAATTGTGGCAAAGAAGGGC
ACATAGCCAGAAATTGCAGGGCTCCTAGGAAAAGGGGGCTGTT
GGAAATGTGGAAAGGAAGGACACCAAATGAAAGATTGTACTG
AGAGACAGGCTAATTTTTTTAGGGAAAATCTGGCCTTCCCACA
AGGGGAGGCCAGGGAACTTTCTTCAGAGCAGGCCAGAACCAA
CAGCCCCCTCTCCAGGGCAGGCCGGAGCCATCAGCCCCGCCAG
AAGAGAGCTTCAGGTTTGGGGAGGAGACAACAACCTCCCTCTC
AGAAGCAGGAGCCGATAGACAGGGACAGGGATCTGTATCCTT
TAGCTTCCCTCAGATCACTCTTTGGCAACGACCCCTCGTCAC
AATAAAGATAGGGGGGGCAGCTGAAGGAAGCTCTATTAGATAC
AGGAGCAGATGATACAGTATTAGAAGACATGCATTTGCCAGG
AAAATGGAAACCAAAAATGATAGGGGGGAATTGGAGGTTTTAT
CAAAGTAAAACAATATGATGAAATTCTTGTAGAAATCTGTGG
ACATAAAGCTATAGGTACAGTATTAGTAGGACCTACACCTGT
CAACATAATTGGAAGAAATCTGTTGACTCAGATTGGTTGCAC
TTTAAATTTTCCCATTAGTCCTATTGAAACTGTACCAGTACA
ATTAAAGCCAGGAATGGATGGCCCAAAGGTTAAACAATGGCC
ATTGACAGAAGAGAAAATAAAAGCATTAGTAGAAATTTGTAC
AGAAATGGAAAAGGAAGGAAAGATTTCAAAAATTGGGCCTGA
AAATCCATACAATACTCCAGTATTTGCCATAAAGAAAAAAGA
TGGTACTAAATGGAGAAAATTAGTAGATTTAGAGACCTTAA
TAAGAGAACTCAAGACTTCTGGGAAGTTCAATTAGGAATACC
ACATCCCTCAGGATTAAAAAAGAAAAAATCAGTAACAGTACT
GGATGTGGGTGATGCATACTTTTCAGTTCCCTTAGATGAAAA
CTTCAGGAAGTATACTGCATTTACCATACCTAGTATAAATAA
TGAGACACCAGGGATTAGATATCAGTACAATGTGCTTCCACA
GGGATGGAAAGGATCACCAGCAATATTCCAAAGTAGCATGAC
AAGAATCTTAGAGCCTTTTAGAAGACAAAATCCAGACATAGT
TATCTATCAATACATGGATGACTTGTATGTAGGATCTGATTT
AGAAATAGGACAGCATAGAATAAAAAATAGAGGAACTGAGACA
ACATCTGTTGAAGTGGGGATTTACCACACCAGACAAAAAGCA
TCAGAAAGAACCCCCATTCTTTGGATGGGTTATGAACTCCA
TCCTGATAAATGGACAGTGCAACCTATAGTACTGCCAGAAAA
AGACAGCTGGACTGTCAATGACATACAGAAGTTAGTGGGTAA
ATTAAATTGGGCAAGTCAGATTTACCCAGGAATTAAAGTAAG
GCAATTATGTAAACTCCTTAGGGGAACCAAAGCACTAACAGA

FIGURE 9

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AGTAATACCACTAACAGAAGAAGCAGAGCTAGAACTGGCAGA
AAACAGGGAAATTCTAAGAGAACCAGTACATGGAGTGTATTA
TGACCCATCAAAAGACTTAATAGCAGAAATACAGAAGCAGGA
GCAAGGCCAATGGACATATCAAATTTATCAAGATCAATTTAA
AAATCTAAAAACAGGAAAGTATGCAAGATTGAGGGGTGCCCA
CACTAATGATGTAAAACAATTTCCAGAGGCAGTGCAAAAAAT
AGCCACAGAAAGCATAGTAATATGGGGAAAGACTCCTAAATT
TAGACTACCCATACAAAAAGAAACATGGGACGCATGGTGGAC
AGAGTATTGGCAAGCCACCTGGATTCTGAGTGGGAGTTTGT
CAATACCCCTCCCCTAGTAAAATTATGGTACCAGTTAGAAAA
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AGCTAACAGAGAGACTAAATTAGGAAAAGCAGGATATGTTAC
TGACAGAGGAAGACAAAAAGTTGTCTCCCTAACTGACACAAC
AAATCAGAAGACTGAGTTACAAGCAATTCATCTAGCTTTGCA
GGATTCAGGATTAGAAGTAAACATAGTAACAGACTCACAGTA
TGCATTAGGAATCATTCAAGCACACCAGATAAAAGTGAATC
AGAAATAGTCAATCAAATAATAGAGCAATTAATAAAAAAGGA
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AGGGAATGAACAAGTAGATAAATTAGTCAGTGCTGGAATCAG
GAAAATACTATTTTTAGATGGAATAGATAAGGCACAAGAAGG
CCATGAGAAATATCACAGTAATTGGAGAGCAATGGCTAGTGG
TTTTAACCTGCCACCTATAGTAGCAAAAGAAATAGTAGCCAG
CTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACA
AGTAGACTGTAGTCCAGGAATATGGCAACTAGATTGTACACA
TCTAGAAGGAAAAATTATCCTGGTAGCAGTTCATGTAGCCAG
TGGATATATAGAAGCAGAAGTTATTCCAGCAGAGACAGGGCA
GGAAACAGCATACTTTATCTTAAAATTAGCAGGAAGGTGGCC
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TACCACGGTTAAGGCCGCCTGTTGGTGGGCAGGGATCAAGCA
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GGAATCTATGAATAGAGAATTAAAGAAAATTATAGGACAGGT
AAGAGATCAGGCTGAACATCTTAAGACAGCAGTACAAATGGC
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ATACAGTGCAGGGGAAAGAATAGTAGACATAATAGCAACAGA
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GAAAGGACCAGCAAACTTCTCTGGAAAGGCCGAAGGGGCAGT
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AAAAGTAAAGATCATTAGGGATTATGGAAAACAGATGGCAGG

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GGAACAGTTT TAGTGAAACACCATATGTATGTTTCAAAGAAAG
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CAAAAATAAGCTCAGAAGTACACATCCCAGTAGGGGAAGCTA
GATTGGTAATAACAACATATTGGGGTCTACATACAGGAGAAA
GAGACTGGCATT TGGGTCAGGGAGTCTCCATAGAATGGAGGG
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CCATAAGAAGTGCCATATTAGGATATAGAGTTAGGCATAGGT
GTGAATATCAAGCAGGACATAACAAGGTAGGATCTCTACAGT
ACTTGGCAC TAACAGCATT AATAACACCAAAGAAGATAAAGC
CACCTTTGCCTAGTGTTGCGAAACTGACAGAGGATAGATGGA
ACAAGCCCCAGAAGACCAAGGGCCACAGAGGCAGCCATACAA
TGAATGGACACTAGAACTTTTAGAGGAGCTTAAGAATGAAGC
TGTTAGGCATTTTCCTAGGGTATGGCTCCATGGCTTAGGGCA
ACATATCTATGAACTTATGGGGATACTTGGGAAGGAGTGGA
GGCCATAACAAGAACTCTGCAACA ACTGCTGTTTATT CATT
CAGAATTGGGTGTCAACATAGCAGAATAGGCATTATT CGACA
GAGGAGAGCAAGAAATGGAGCCAGTAGATCCTAGACTAGAGC
CCTGGAAGCATCCAGGAAGTCAGCCTAAGACTGCGTGTACCA
CTTGCTATTGTAAAAAGTGCTGCTTTCATTGCCAAGTTTGTT
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AAGCTTATCTATCAAAGCAGTAAGTAATATATGTAATGCAAC
CTTTACAAATAGTAGCAATAGTAGCATTAGTAGTAGCAGGAA
TAATAGCAATAGTTGTGTGGACCATAGTATTCATAGAATATA
AGAAAATATTAAGACAAAGAAAAATAGACAGGTTGATTGATA
GAATAAGAGAAAGAGCAGAAGACAGTGGCAATGACAGTGAAG
GGGATCAGGAAGAATTATCGGCACTTGTGGACATGGGGCACC
ATGATCCTTGGGATATTAATGATCTGTAGAGCTGCAAACAAT
TTGTGGGT CACAGTCTATTATGGGGTACCTGTGTGGAGAGAA
GCAACCACCACTCTATTTTGTGCATCAGATGCCAAGGCATAT
GATGCAGAGGTACATAATGTTTGGGCCACACATGCCTGTGTA
CCCACAGACCCTAACCACAAGAAGTAGAATTGAAAAATGTG
ACAGAAAATTTTAACATGTGGAAAAATAACATGGTAGAACAG
ATGCATGAGGATATAATCAGTTTATGGGATCAAAGCCTGAAG
CCATGTGTAAAATTAACCCCACTCTGTGTTTCTTTAAATTGC
ACTGATGCTACTAATACCACTAATAGTAATACCACTAGCAGC
AGCGAGAAACCGAAGGGGACAGGGGAAATAAAAAACTGCTCT

FIGURE 9

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TTCAATATCACCACAAGCATAAGAGATAAGGTGCAGAAACAA
TATGCACTTTTTTTATAGCCTTGATGTAGTACCAATGGATGAT
AATGATAATAGTACAAGCTATAGGTTAATAAGTTGTAACACC
TCAATCATTACACAGGCCTGTCCAAAGATATCCTTTGAGCCA
ATTCCCATAACATTATTGTGCCCCGGCTGGTTTTGCGATTCTA
AAGTGTAAGATAAAAGGTTCAATGGAAAAGGACCATGTACA
AGTGTCAGCACAGTACAGTGTACACATGGAATTAGGCCAGTA
GTATCAACTCAACTGTTGTAAATGGCAGTCTAGCAGAAGAA
GAGGTAGTAATTAGATCTGACAATTTTACGAACAATGCTAAA
ACCATAATAGTACAGCTGAGCAAATCTGTAGAAATTACTTGT
GTAAGACCCCAACAACAATACAAGAAAAAGTATAAGTATGGGA
CCAGGGAGAGCATTTTATACAACAGAAATAATAGGAGATATA
AGCAAGCATATTGTAACATTAGTAAAGCAAAGTGGACTGAC
ACTTTAGAACAGATAGCTAGAAAATTAAGAGAACAATTTGAG
AATAAAACAATAGTCTTTAAGCCATCCTCAGGAGGGGACCCA
GAAATTGTAACACAGTTTTTACAGTTTTTAATTGTGGAGGGGAA
TTTTTCTACTGTAATTCAACACAAGTGTTTAATGGTACTTGG
AATGGTACTTGGGTTAATGGTACTTGGAGTAGTAATAATACG
ACTGATACTGCAAATATCACACTCCCATGCAGAATAAAACAA
TTTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCC
CCTCCCATCAAAGGACAAATTAATGTACATCAAATATTACA
GGGCTGATATTAACAAGAGATGGTGGTAACAATAACACCACG
AACGACAACGAGACCGAGACCTTCAGACCTGGAGGAGGAGAT
ATGAGGGACAATTGGAGAAGTGAATTATATAAATATAAAGTA
GTACAAGTTGAACCATTAGGAGTAGCACCCACCAAGGCAAAG
AGAAGAGTGGTGCAAAGAGAGAAAAAGAGCAGTGGGAATAGGA
GCTATGTTCCCTTGGGTTCTTAGGAGCAGCAGGAAGCACTATG
GGCGCAGCGTCAGTGACGCTGACGGTACAAGCCAGACAATTA
TTGTCTGGTATAGTGCAGCAGCAGAACAATCTGCTGAGGGCT
ATTGAGGGCGCAACAGCATCTGTTGCAACTCACAGTCTGGGGC
ATCAAACAGCTCCAGGCAAGAGTCCTGGCTGTGGAAAGATAC
CTAAGGGATCAACAGCTCCTGGGACTTTGGGGTTGCTCTGGA
AACTCATTTCACCACTACTGTGCCTTGGAACAATAGCTGG
AGTAATAAATCTCTGGAAACAATTTGGGATAACATGACCTGG
ATGCAGTGGGAAAGAGAAATTGACAATTACACAAACATAATA
TACACCTTAATTGAAGAATCGCAGAACCAACAAGAAAAAAT
GAACTAGAATTATTGGAATTGGATAAATGGGCAAATTTGTGG
AATTGGTTTAGTATATCAAAGTGGCTATGGTATATAAAATTA
TTCATAATGGTAGTAGGAGGCTTGGTAGGTTTAAGAATAGTT

FIGURE 9

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TTTACTGTACTTTCTATAGTTAATAGAGTTAGGCAGGGATAC
TCACCATTATCGTTTCAGACCCACCTCCCAACCCCGAAGGGA
CCCGACAGGCCAGAAGGAATCGAAGAAGAAGGTGGAGAGAGA
GACAGAGGCAGCTCCACTCGATTAGTGCACGGATTCTTAGCA
CTTTTCTGGGACGACCTGAGGAGTCTGTGCCTCTTCAGCTAC
CACCACCTTGAGAGACTTACTCTTGATTGTAACGAGGATTGTG
GAACTTCTGGGACGCAGGGGATGGGAAGCCCTCAAATACTGG
TGGAATCTCCTGCAGTATTGGAGGCAGGAACACTACAGAAGAGT
GCTGTTAGCTTGTTCAATGGCACGGCCATAGCAGTAGCTGAG
GGGACAGATAGAGTTATAGAAGCTTTACGAAGGGCTTATAGA
GCTATTCTCCACATACCTAGAAGAATAAGACAGGGGCTTAGAA
AGGGCTTTGCTATAAAATGGGTGGCAAGTGGTCAGAAAGTAG
TGTGGTTAGAAGGCATGTACCTTTAAGACAAGGCAGCTATAG
ATCTTAGCCGCTTTTTTAAAGAAAAGGGGGGACTGGAAGGGC
TAATTCACCTCACGGAAAAGACCAGTTGAACCAGAAGAAGATA
GAAGAGGCCATGAAGAAGAAAACAACAGATTGTTCTGCTTGC
TCAGCTGGGGACTTTCCAGAAGGCGCGGCCTGAGTGACTAAG
CCCCGTTGGGGACTTTCCGAAGAGGCATGAAGGGACTTTCCA
AGGCAGGCGTGGCCTGGGCGGGACTGGGGAGTGGCGAGCCCT
CAGATGCTGCATATAAGCAGCTGCTTTCTGCCTGTACTGGGT
CTCTCTGGTTAGACCAGATCTGAGCCTGGGAGCTCTCTGGCT
AGCTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTT
GAGTGCTTCAAGTAGTGTGTGCCCCGTCTGTTGTGTGACTCTG
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TCTCTAGCA

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trends in CD3 count since seroconversion

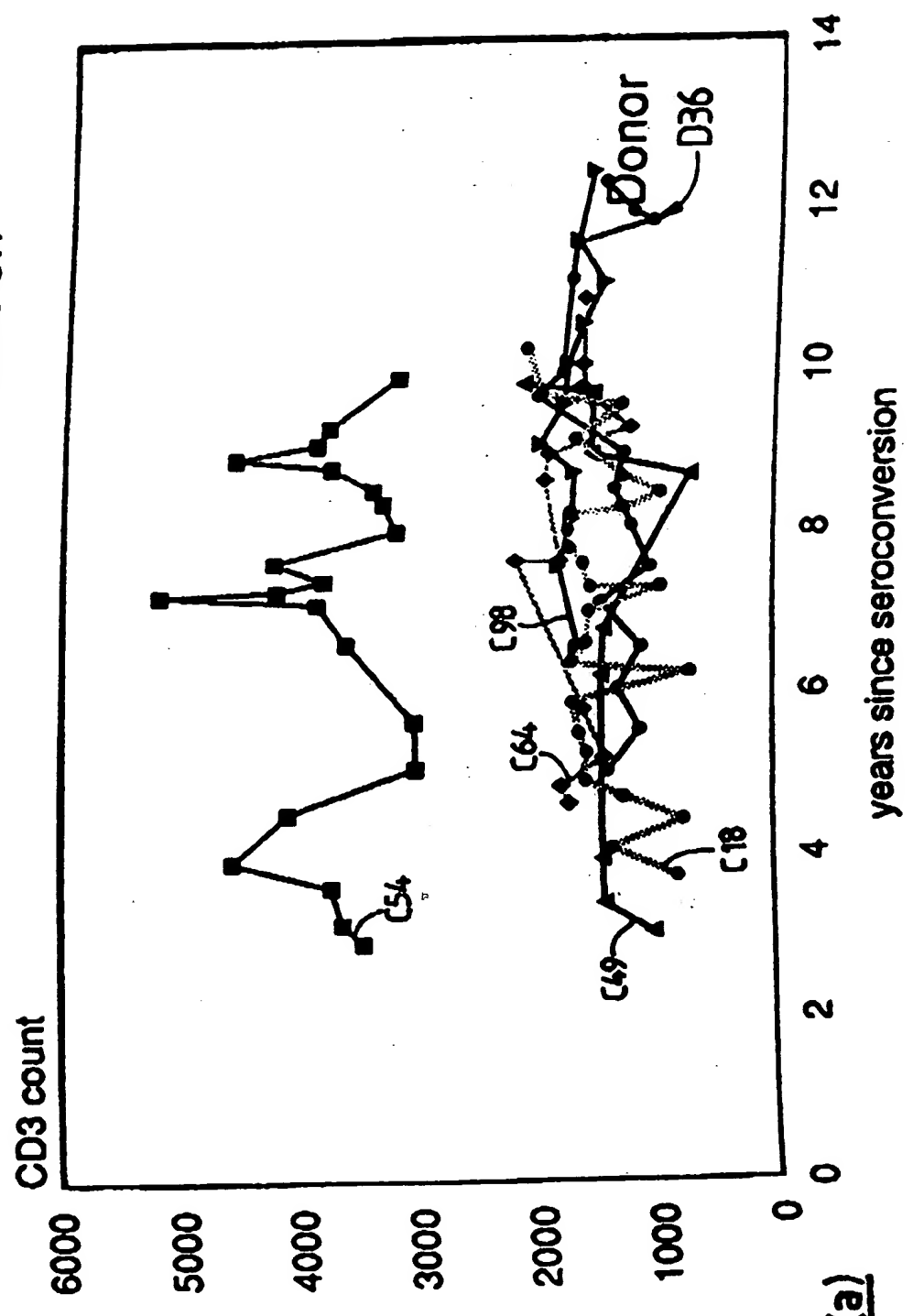
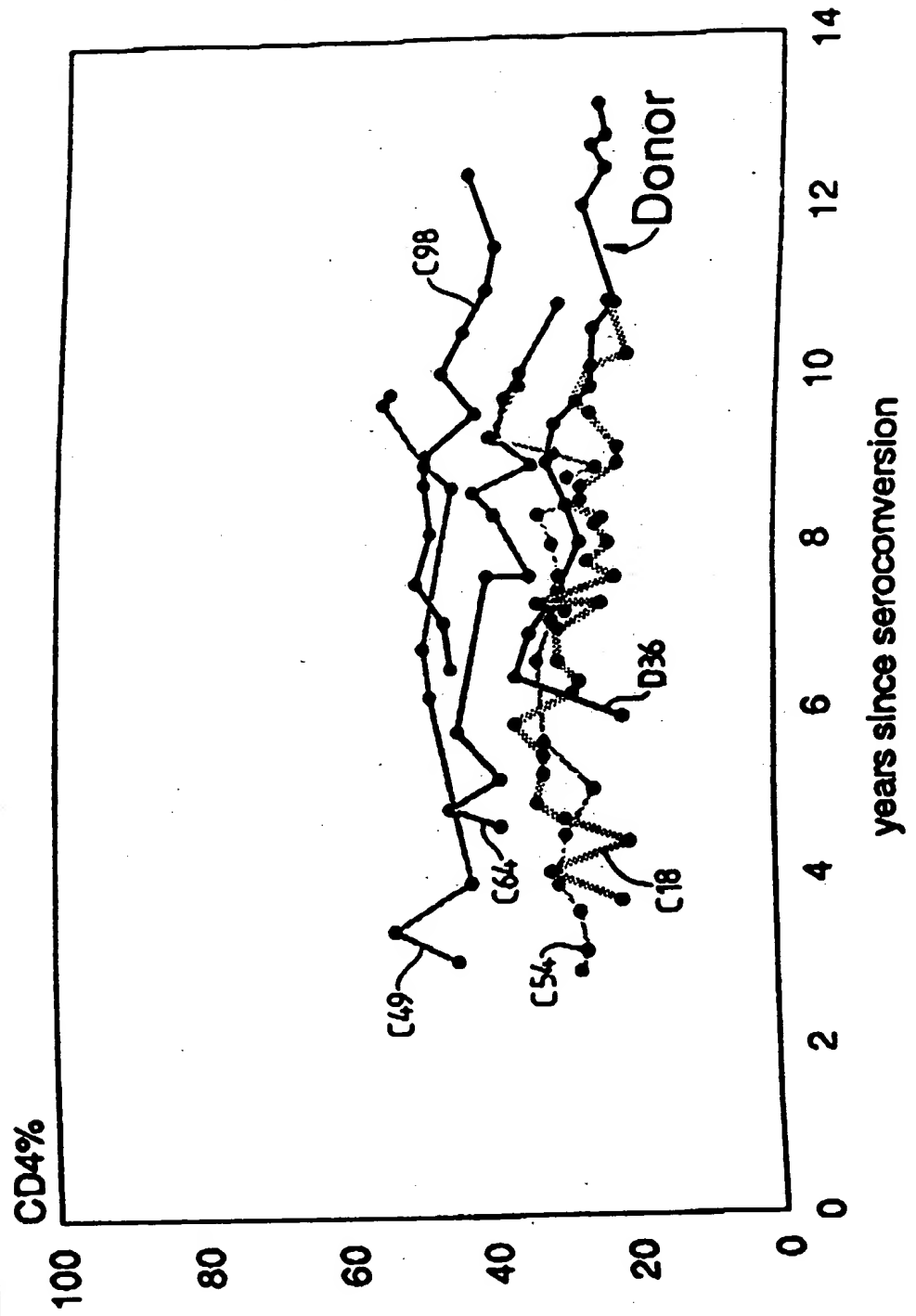


FIG 10(a)

FIG 10(b)(ii) trends in CD4% since seroconversion



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FIG 10(c)(i) trends in CD8 since seroconversion

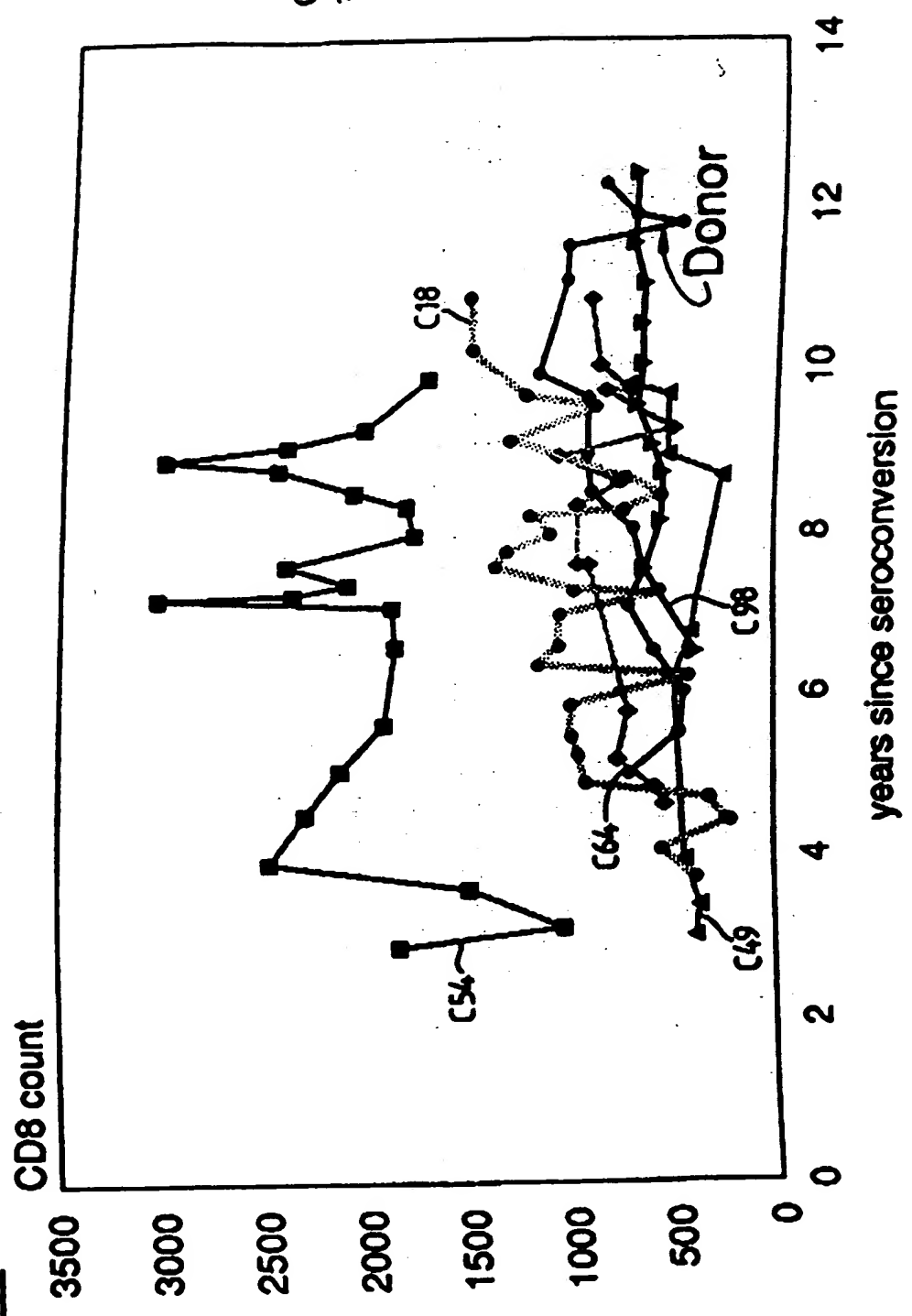
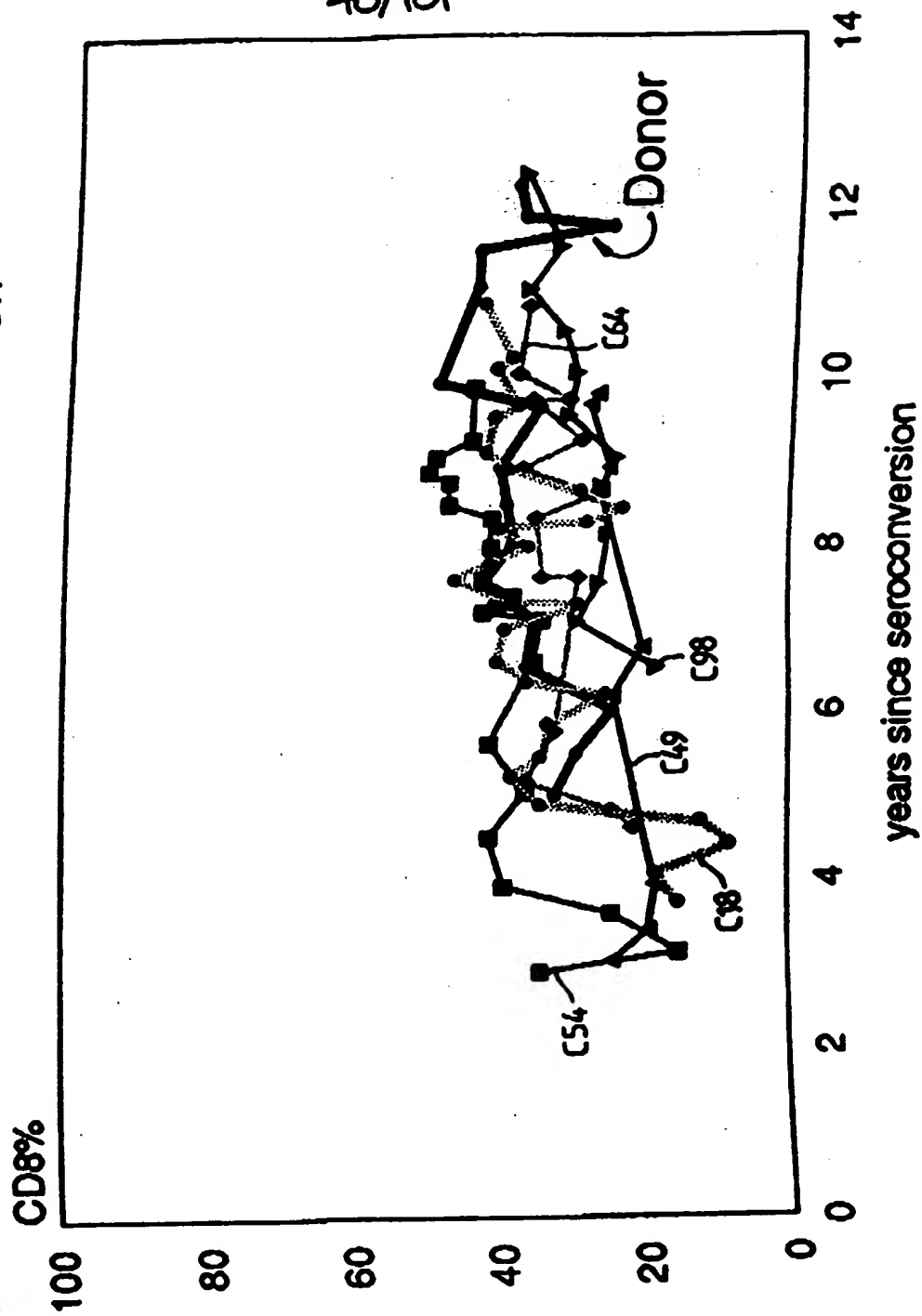


FIG 10 (c) (ii)



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FIG 10 (d) trends in lymphocyte count since seroconversion

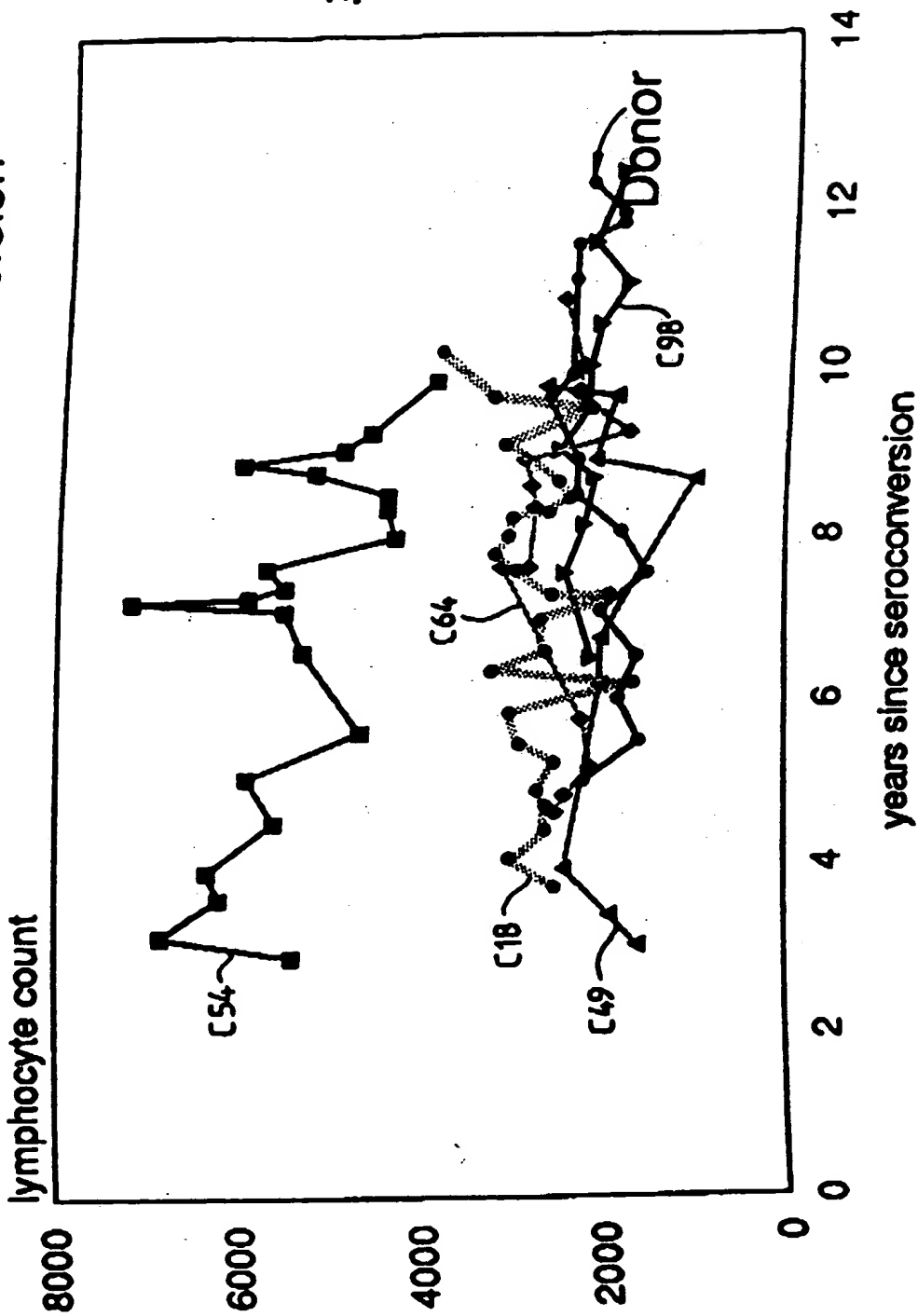
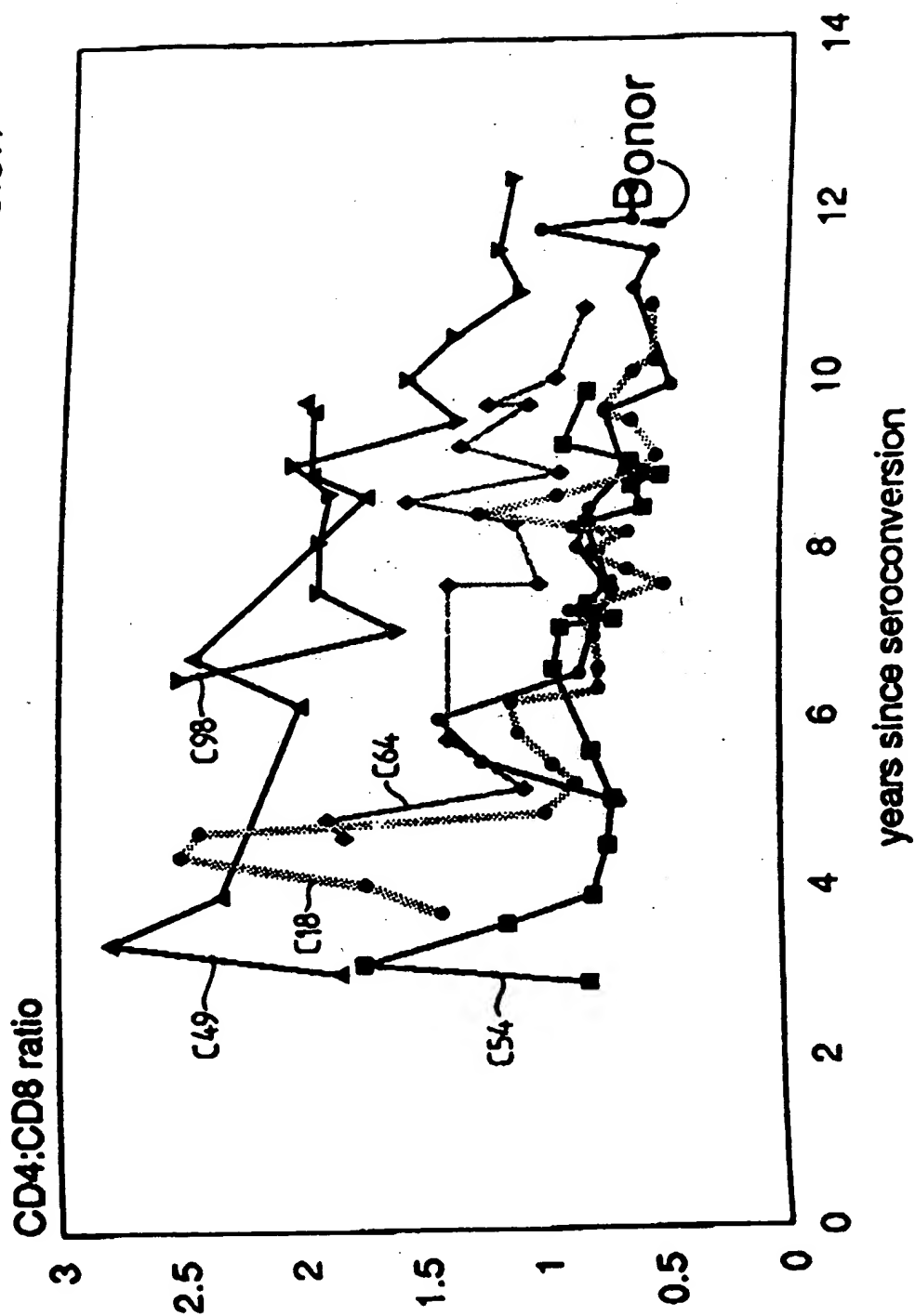


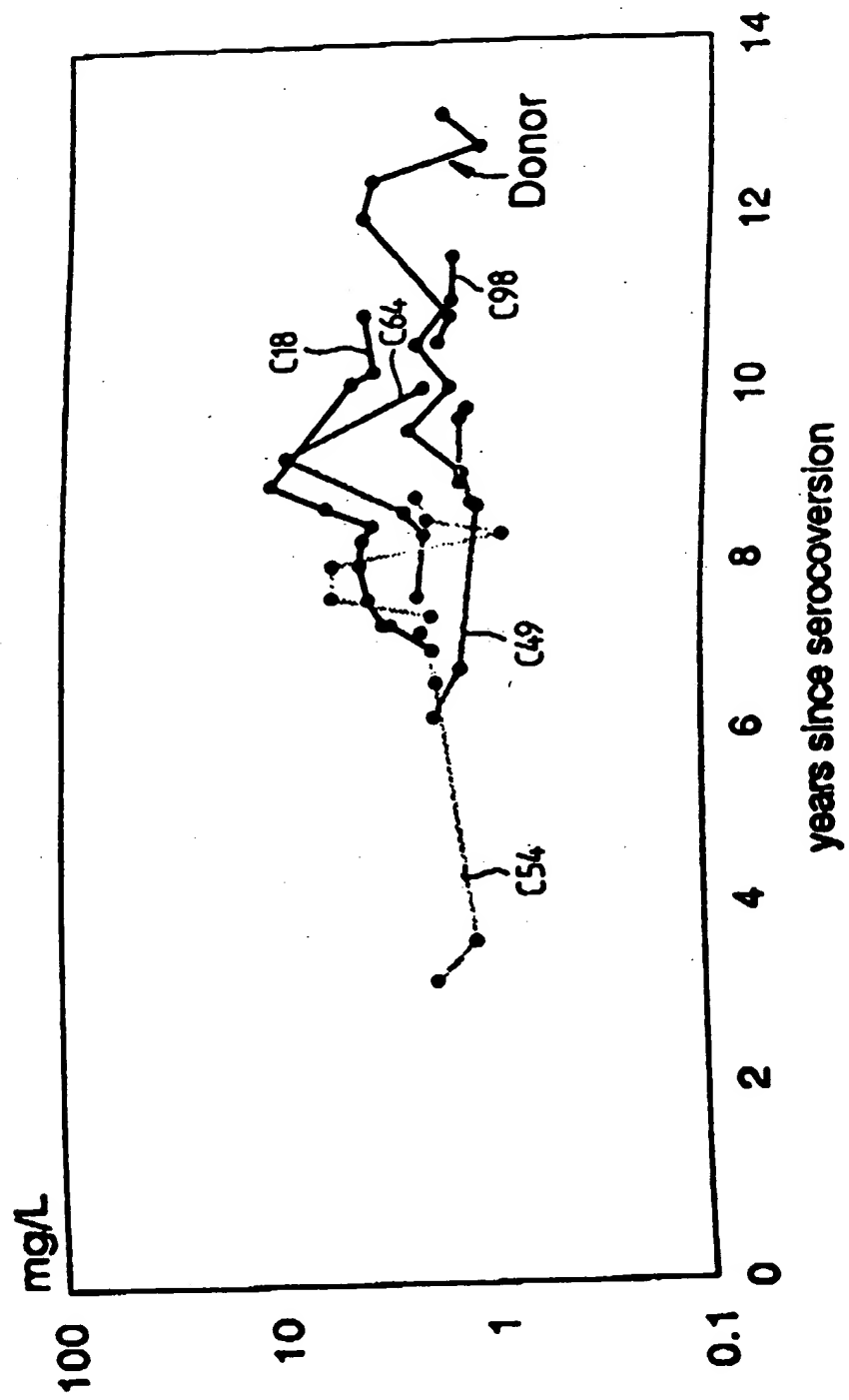
FIG 10(e) trends in CD4:CD8 ratio count since seroconversion



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trends in beta-2 microglobulin since seroconversion

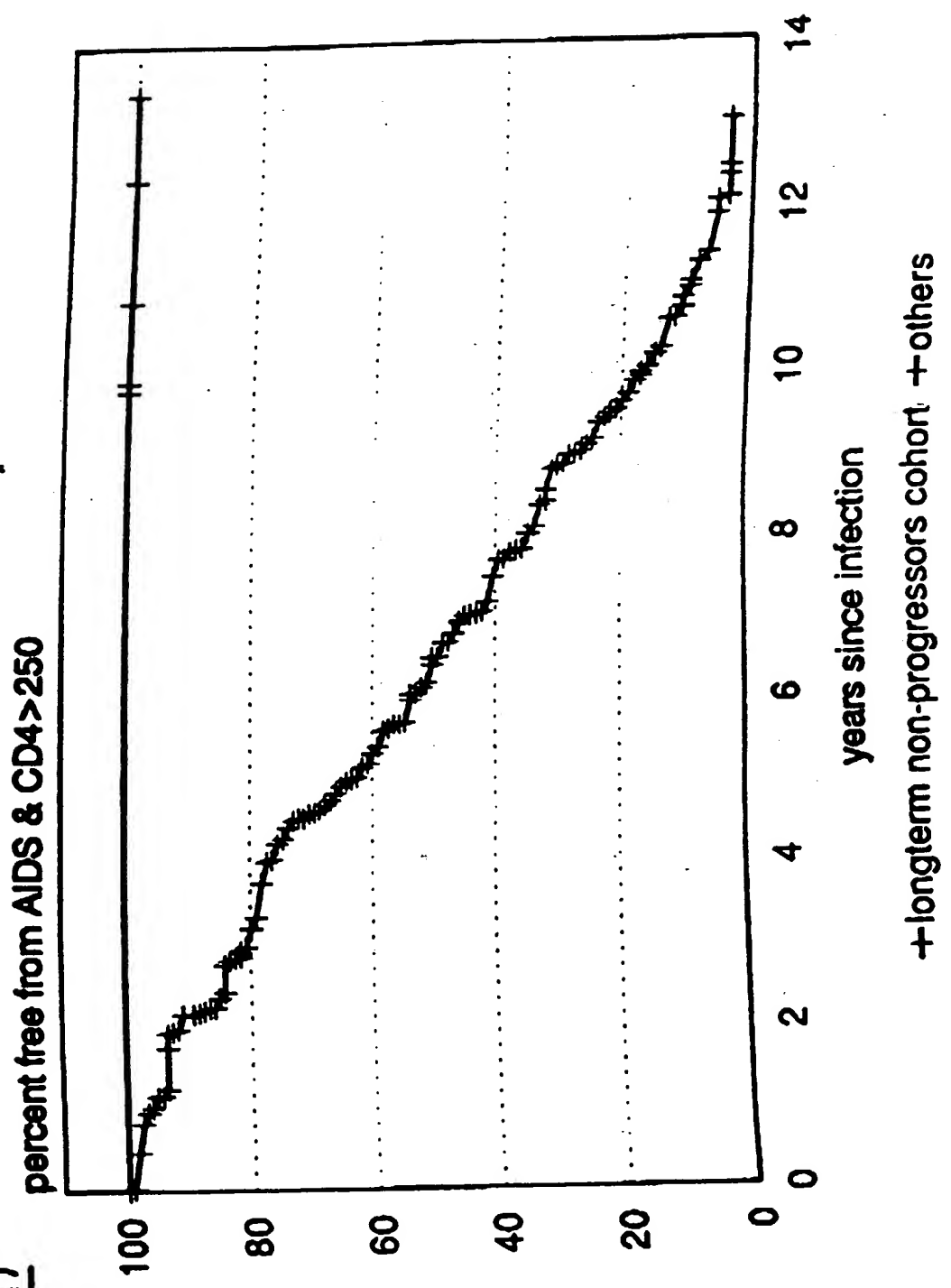
FIG 10 (f)



beta-2 microglobulin plotted on a log scale

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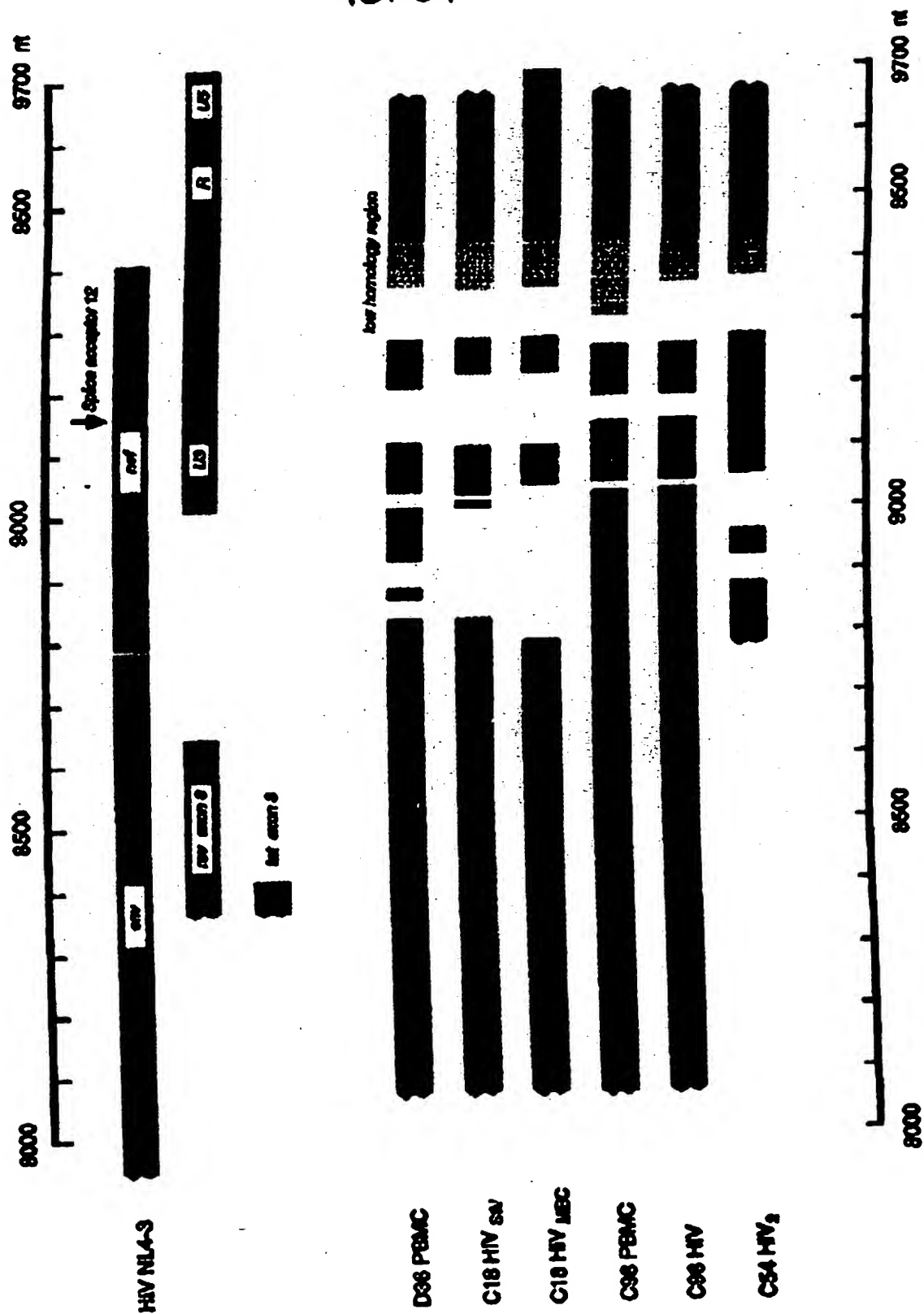
FIG 10(g)



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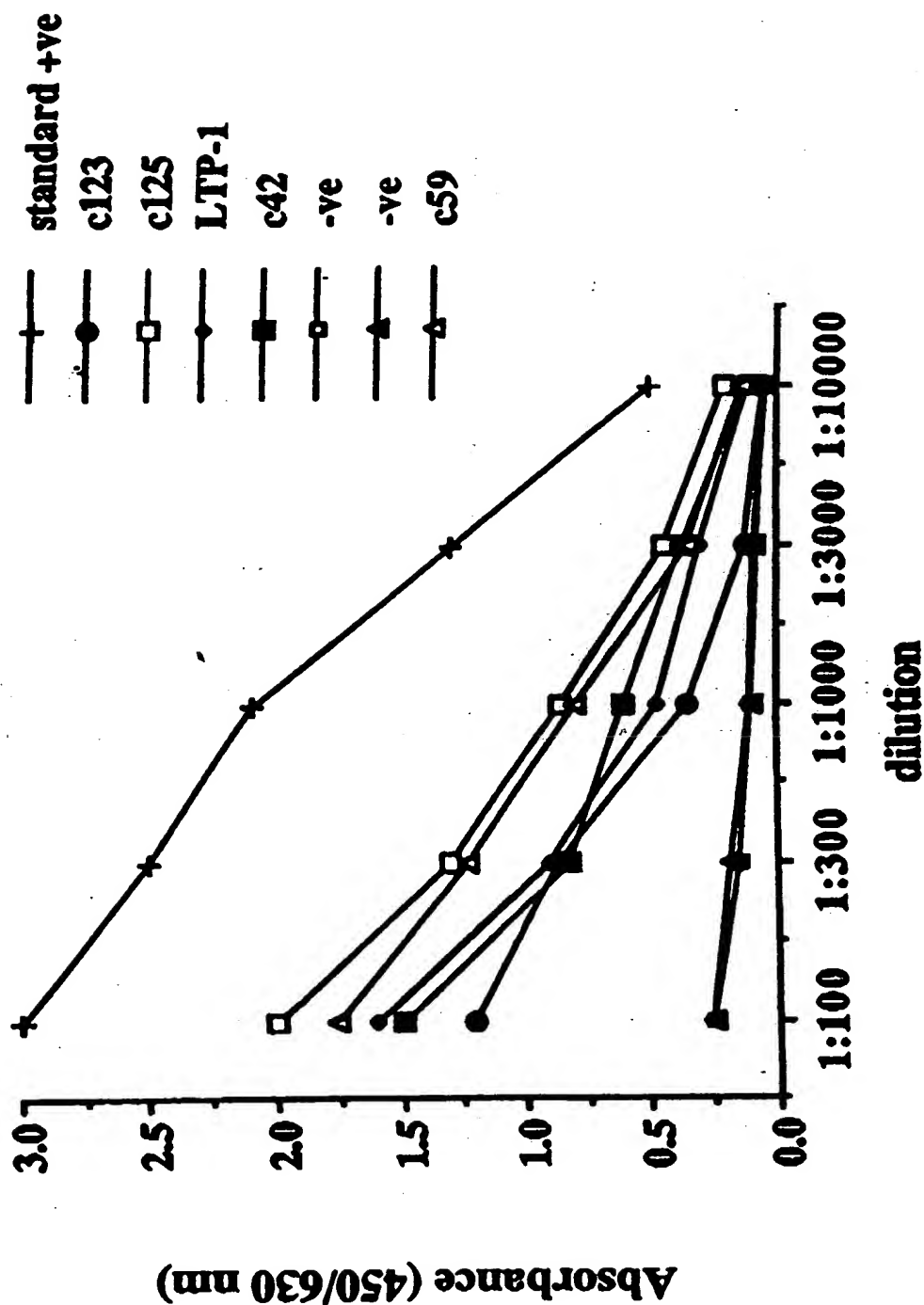
FIGURE 11

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FIGURE 12A

LTP.control gp vs Nef 27

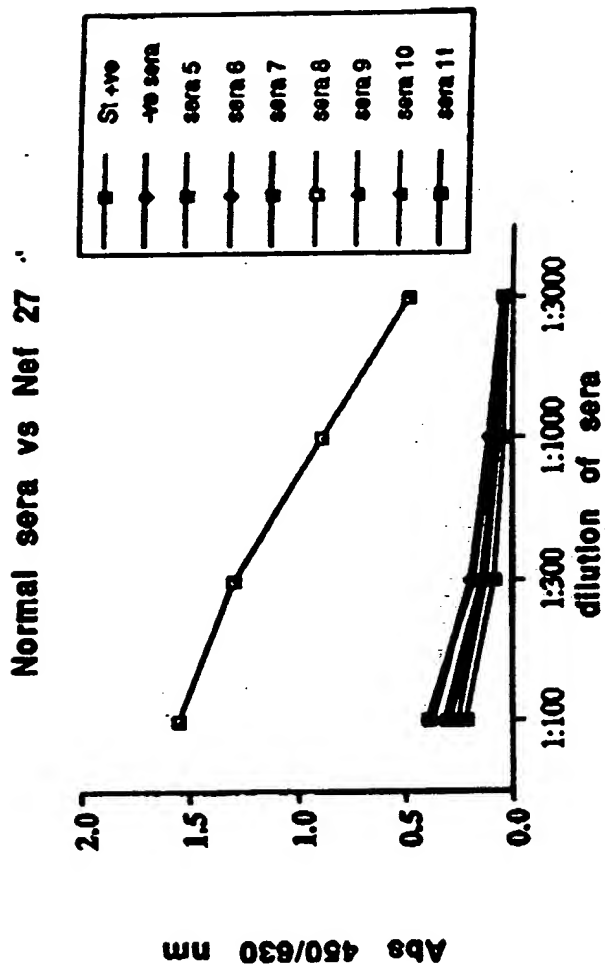


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Normal sera vs Nef 27

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FIGURE 12B(i)



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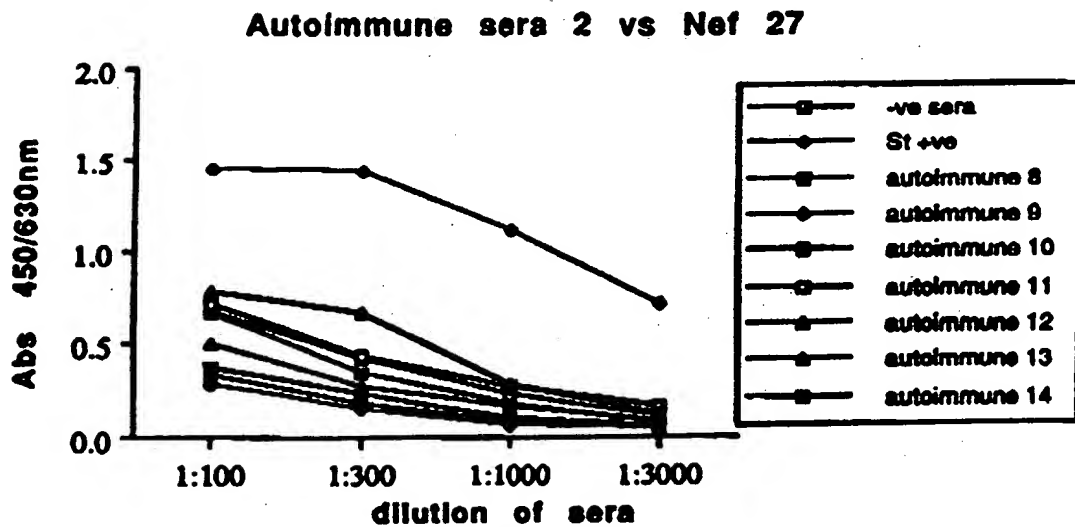
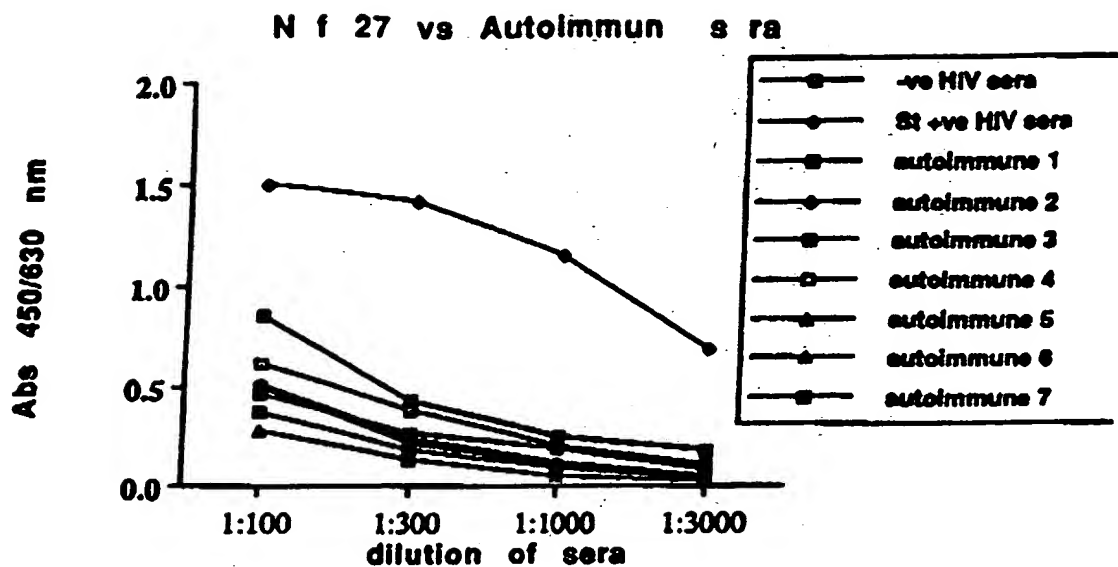
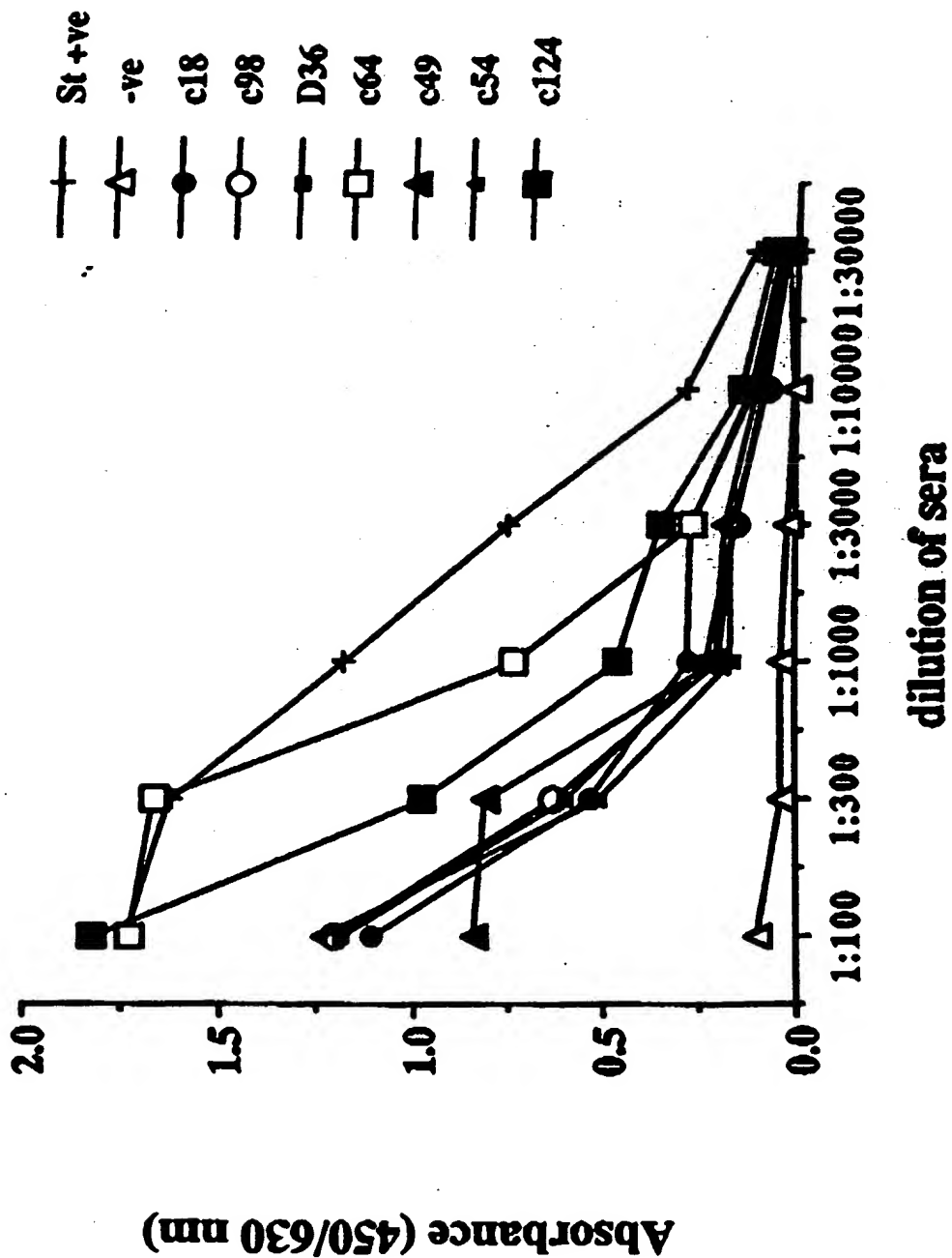


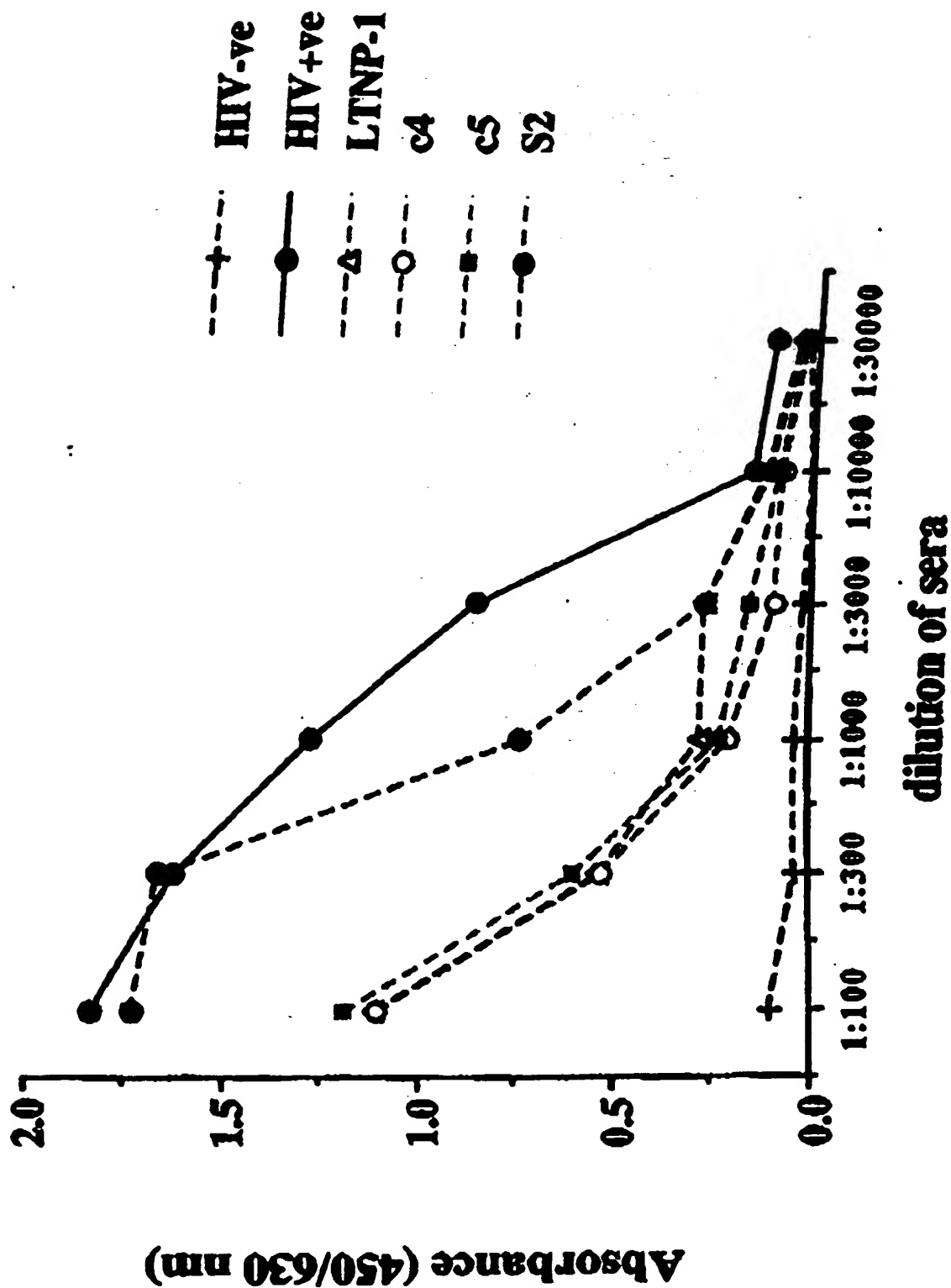
FIGURE 12B(ii)

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FIGURE 12D

Non-progressor sera vs Nef 27

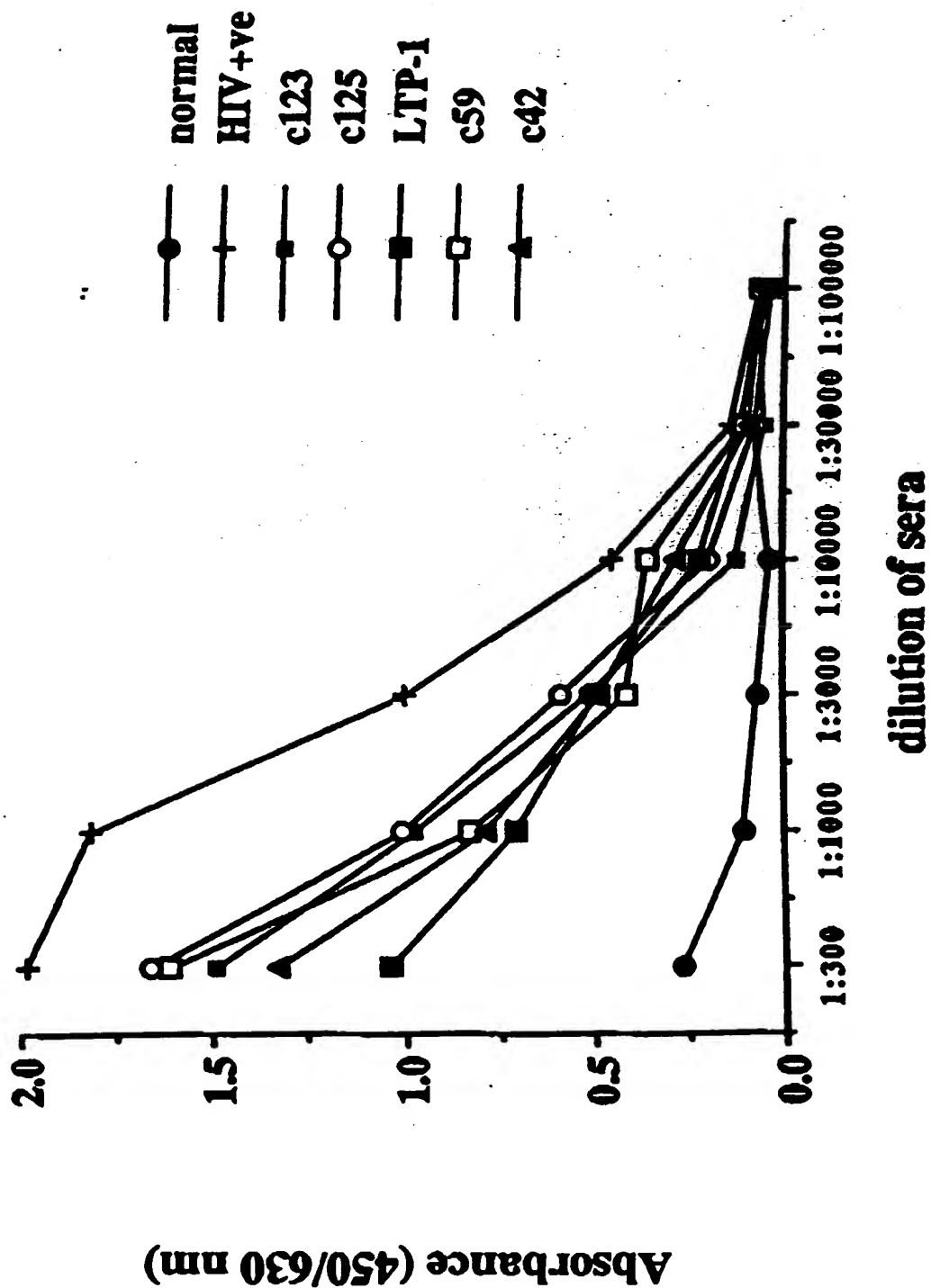


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LTP gp.vs Nef aa1-19

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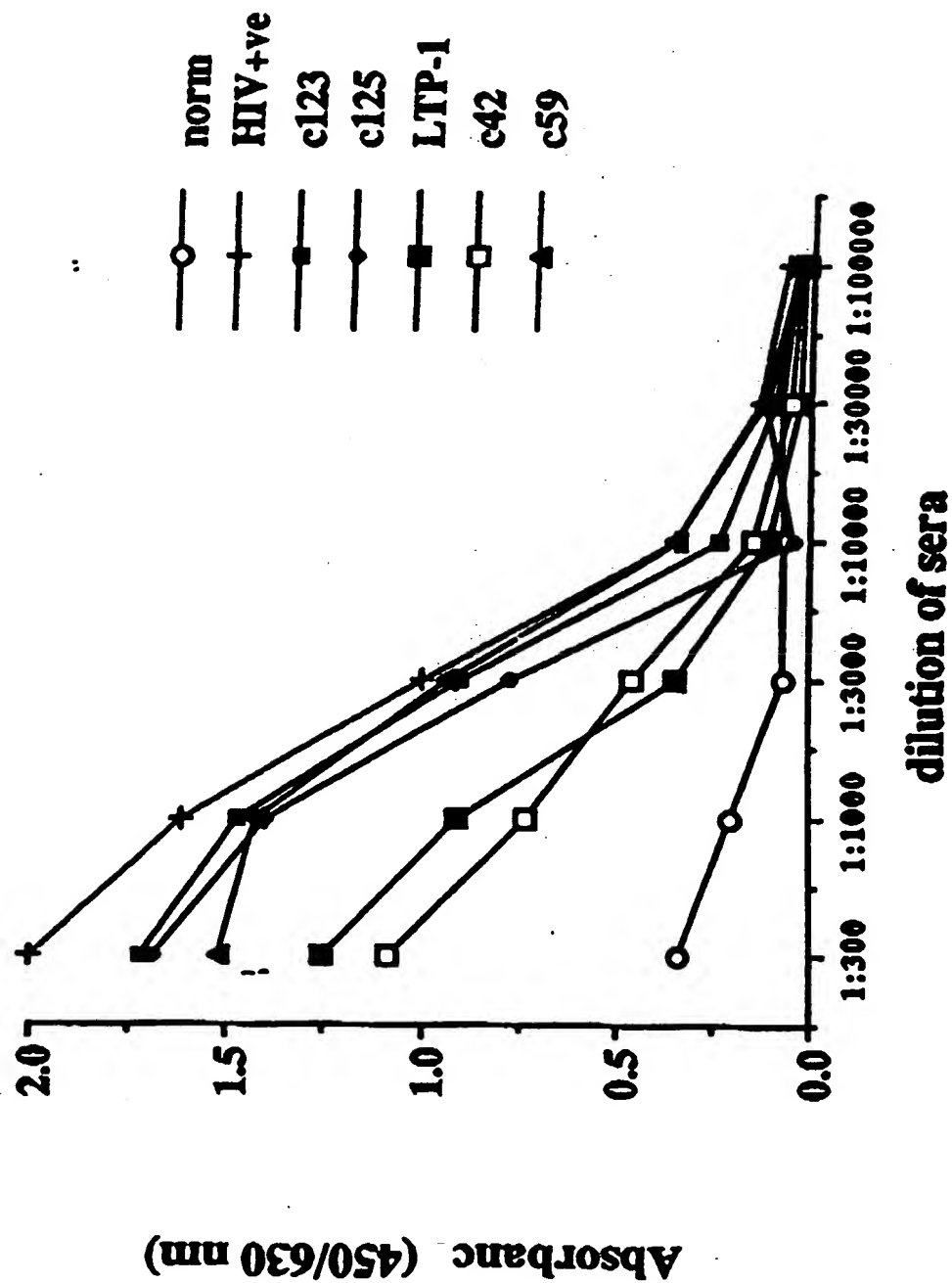
FIGURE 13A(i)



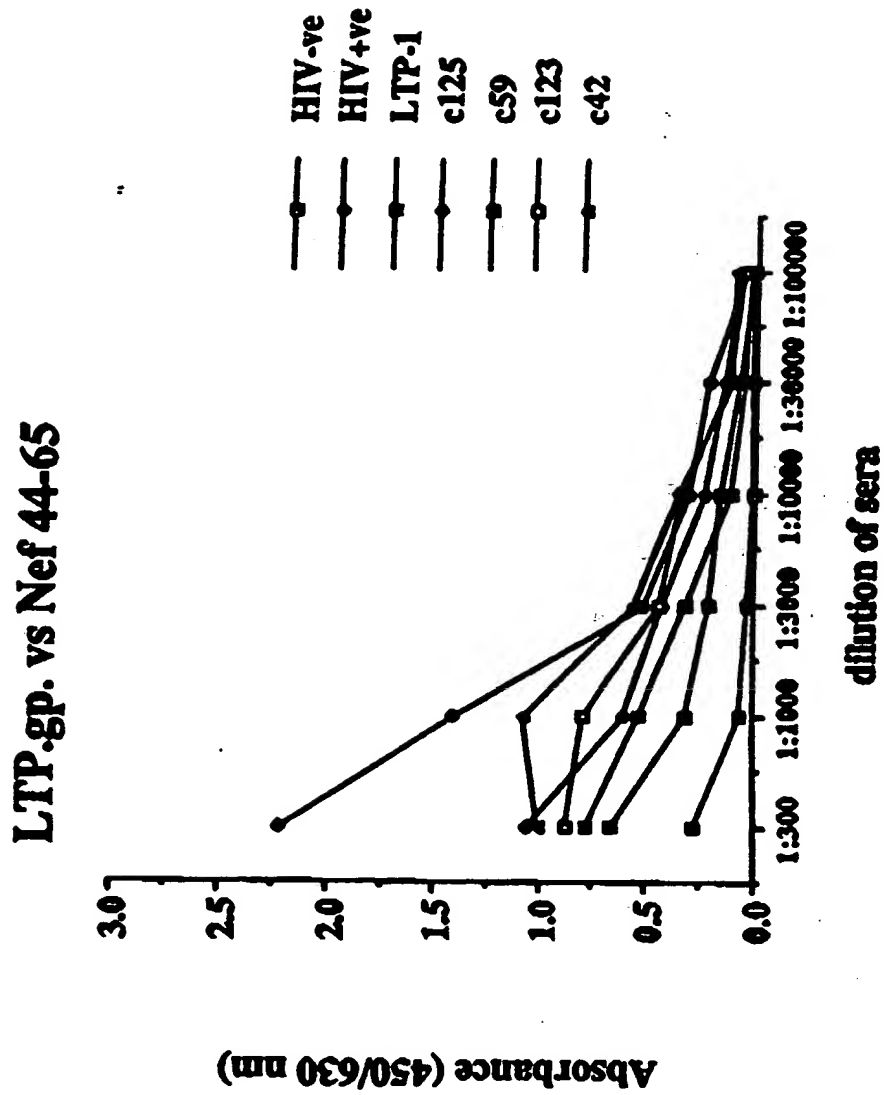
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FIGURE 13A (ii)

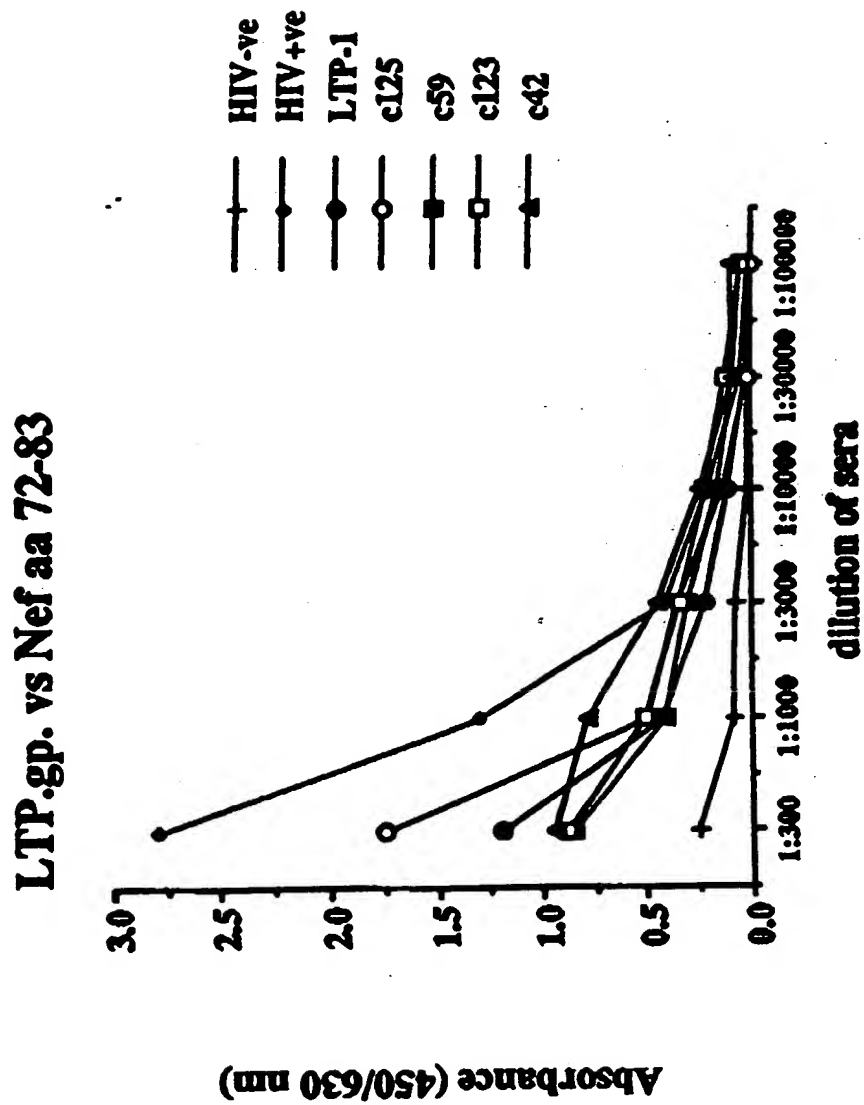
LTP.gp vs Nef aa 20-36



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FIGURE 13A (iii)

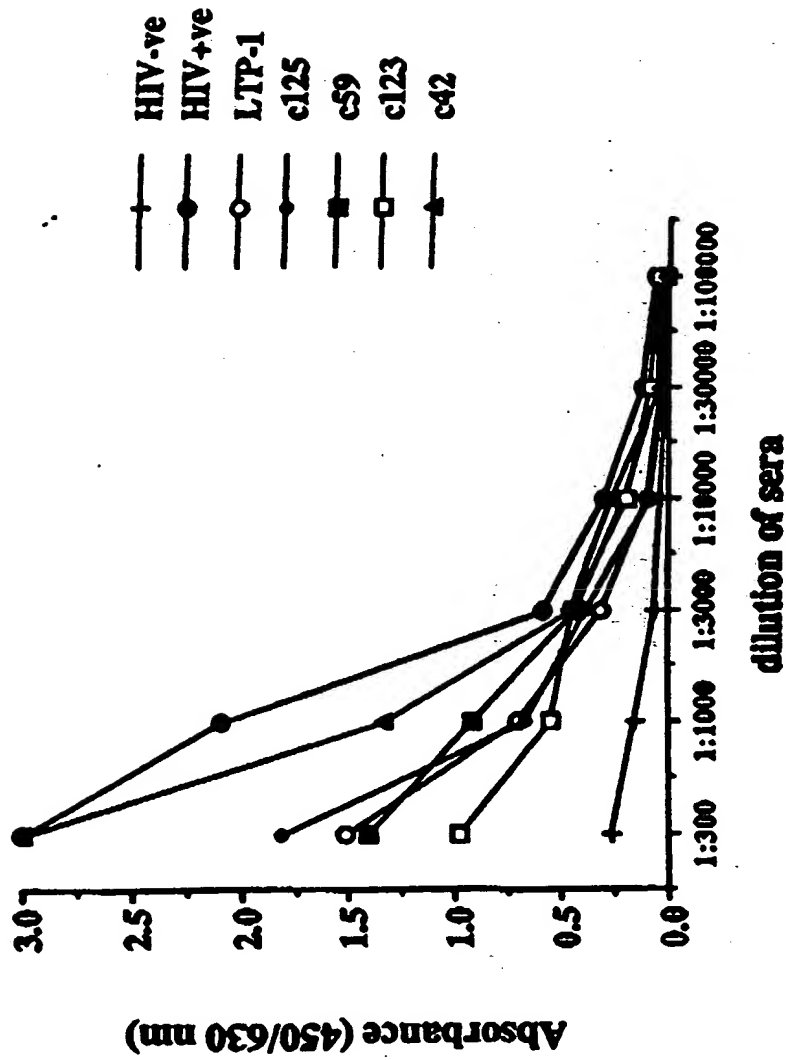


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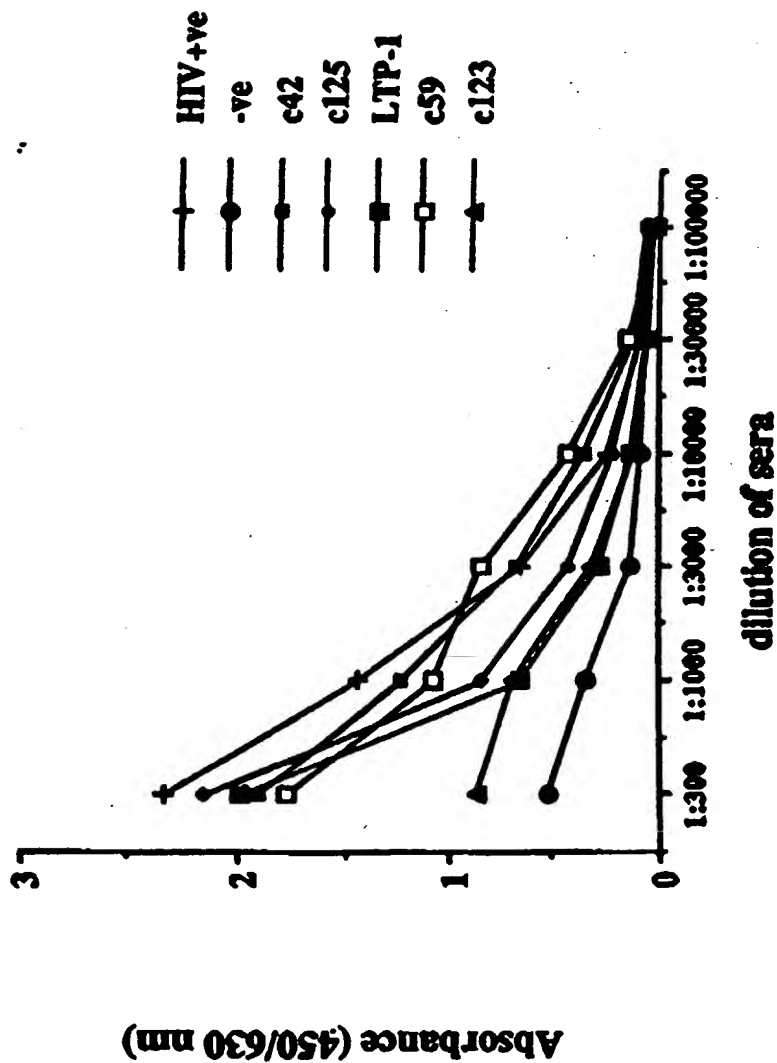
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FIGURE 13A (v)

LTP.gp. vs Nef aa 89-97



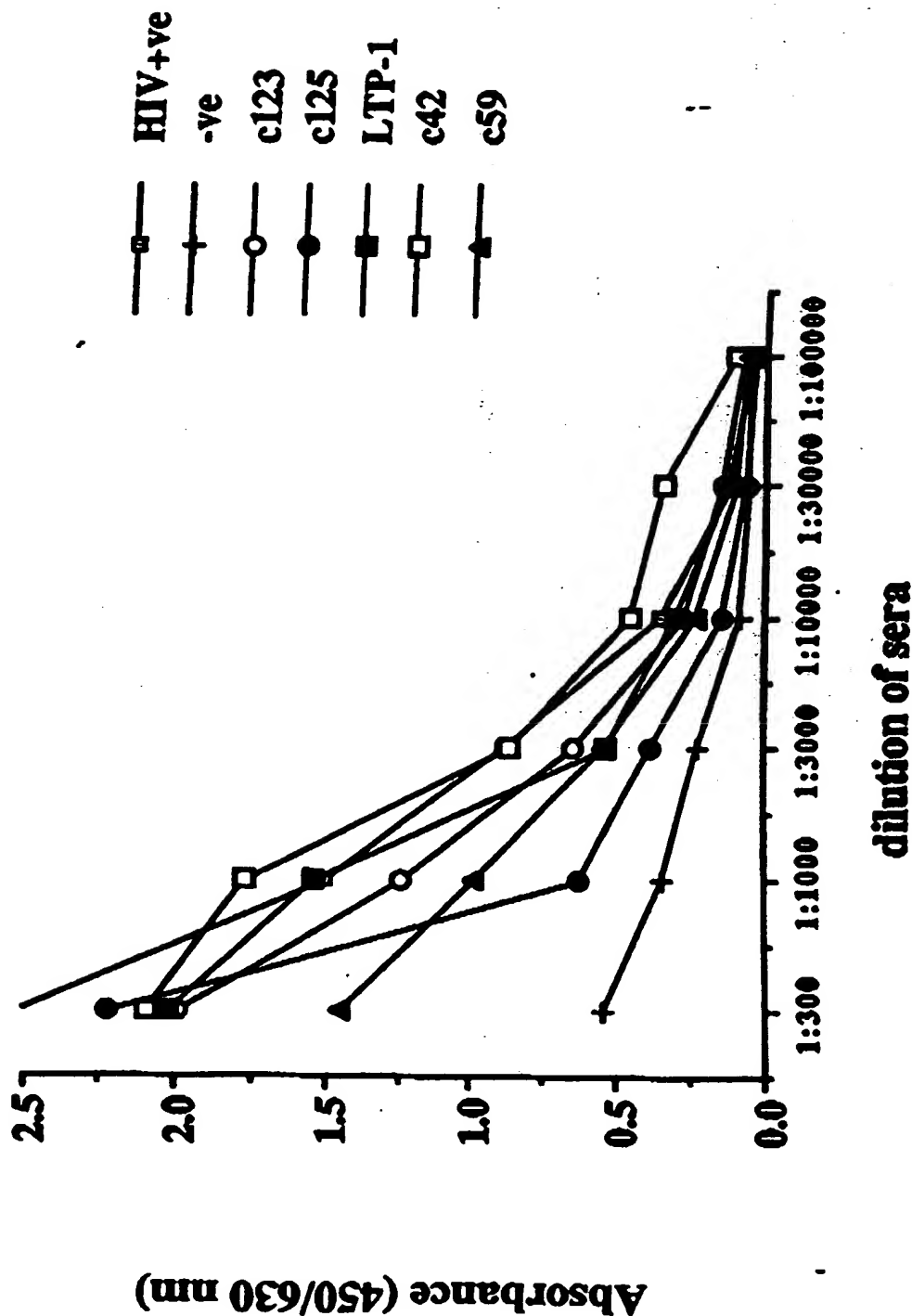
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FIGURE 13A (ii)

LTP gp.vs Nef aa 121-135



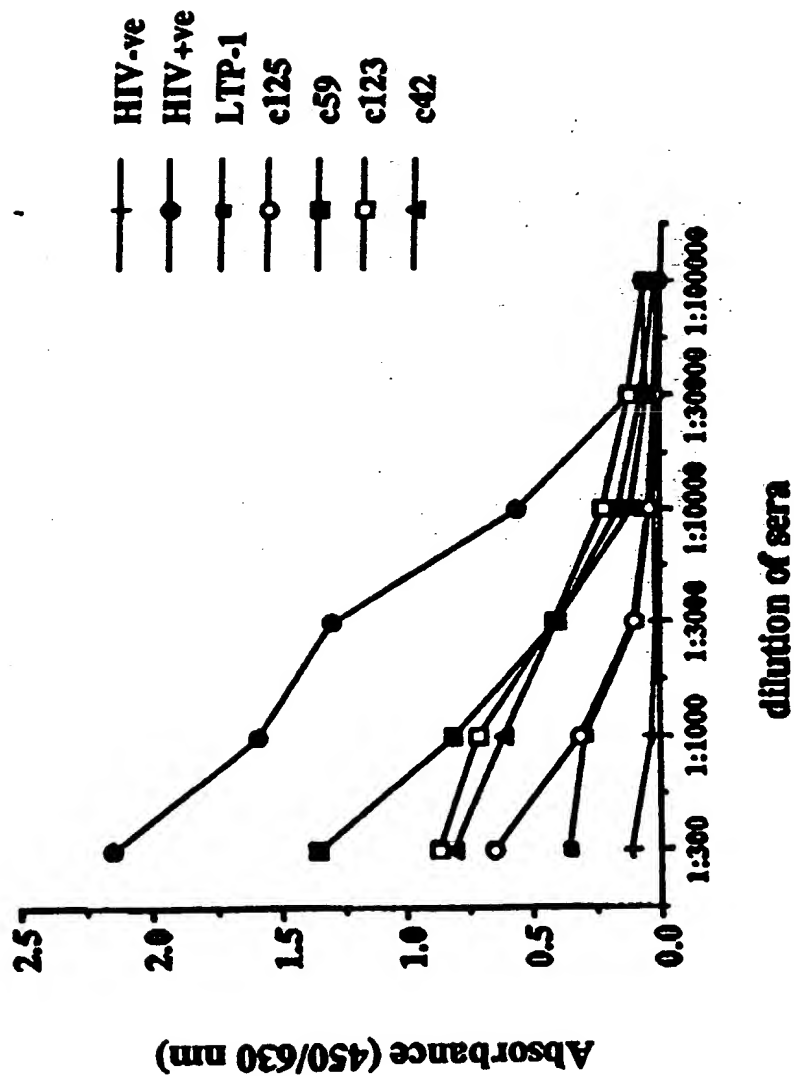
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FIGURE 13A (vii)

LTP.gp vs Nef 162-177



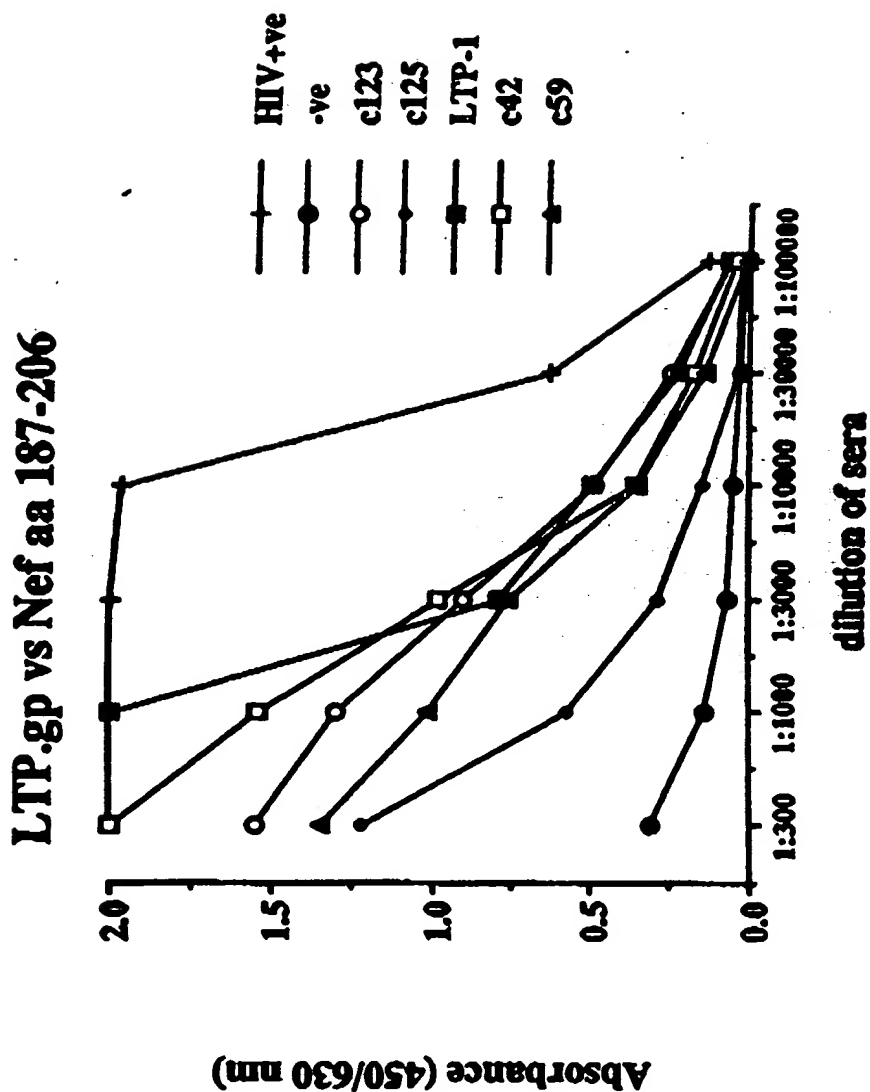
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FIGURE 13A (ik)

LTP.gp. vs Nef 164-186

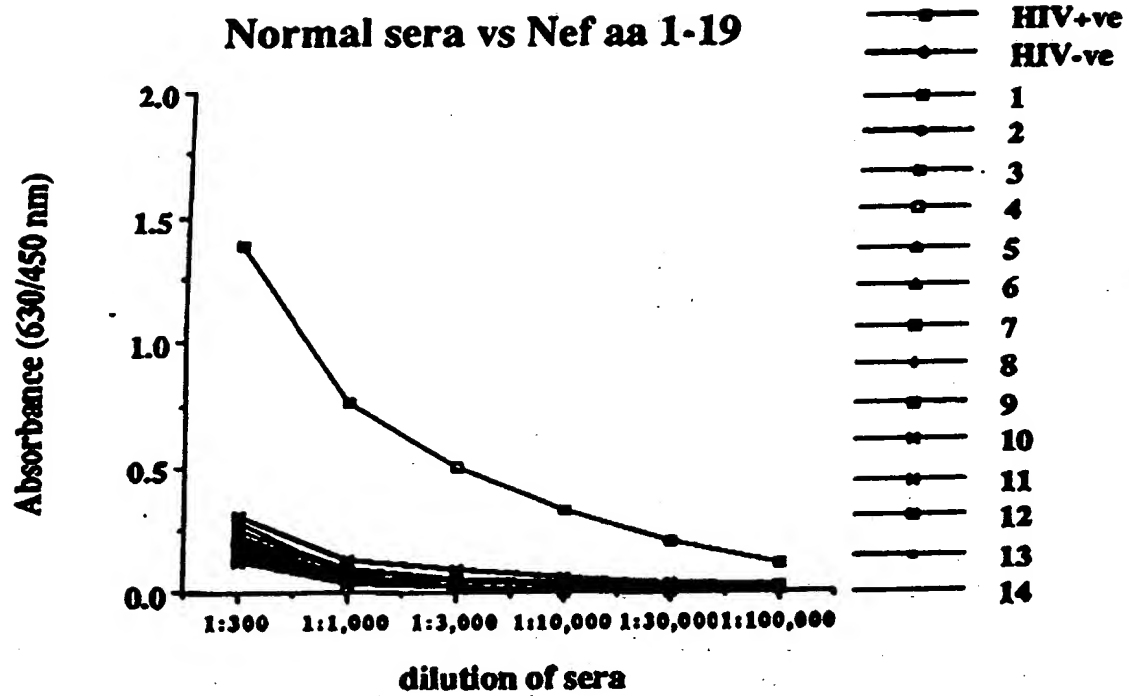


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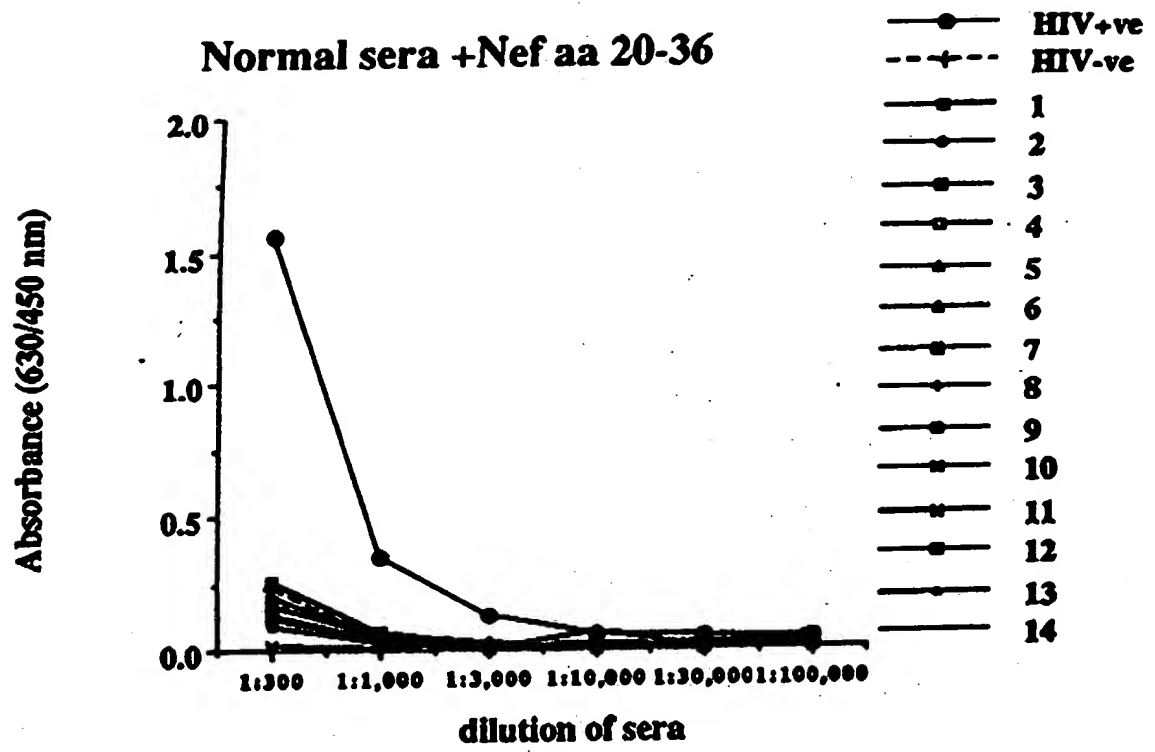
FIGURE 13A(x)



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FIGURE 13B (i) (ii)



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FIGURE 13B (i) (ii)

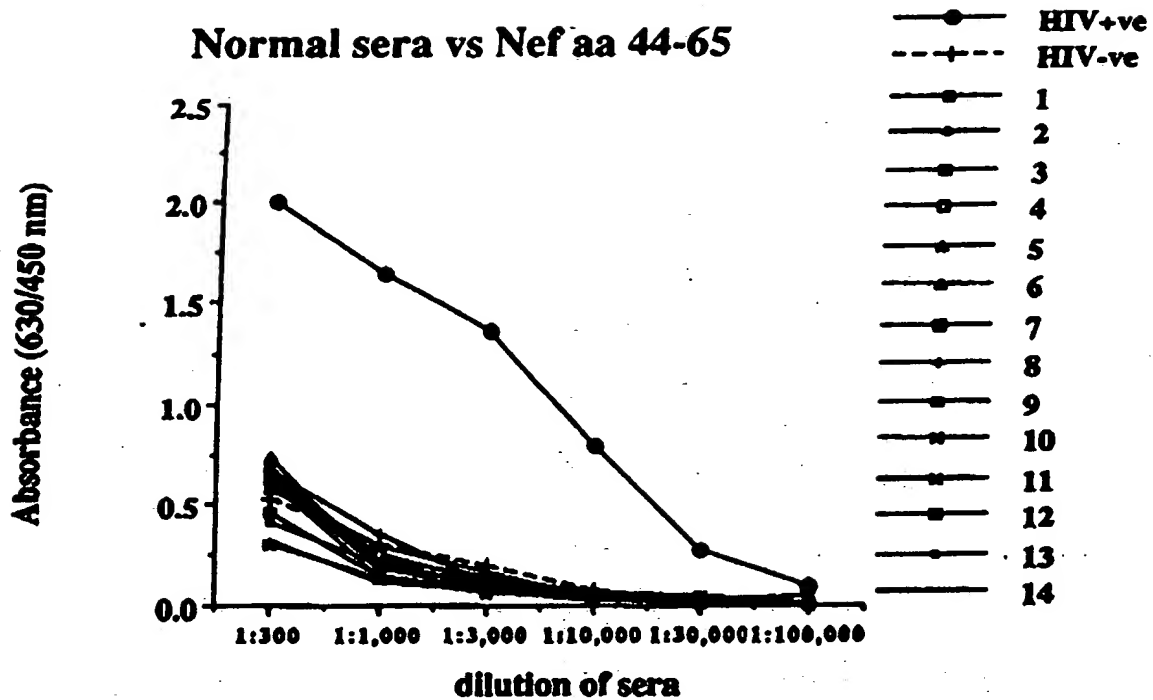
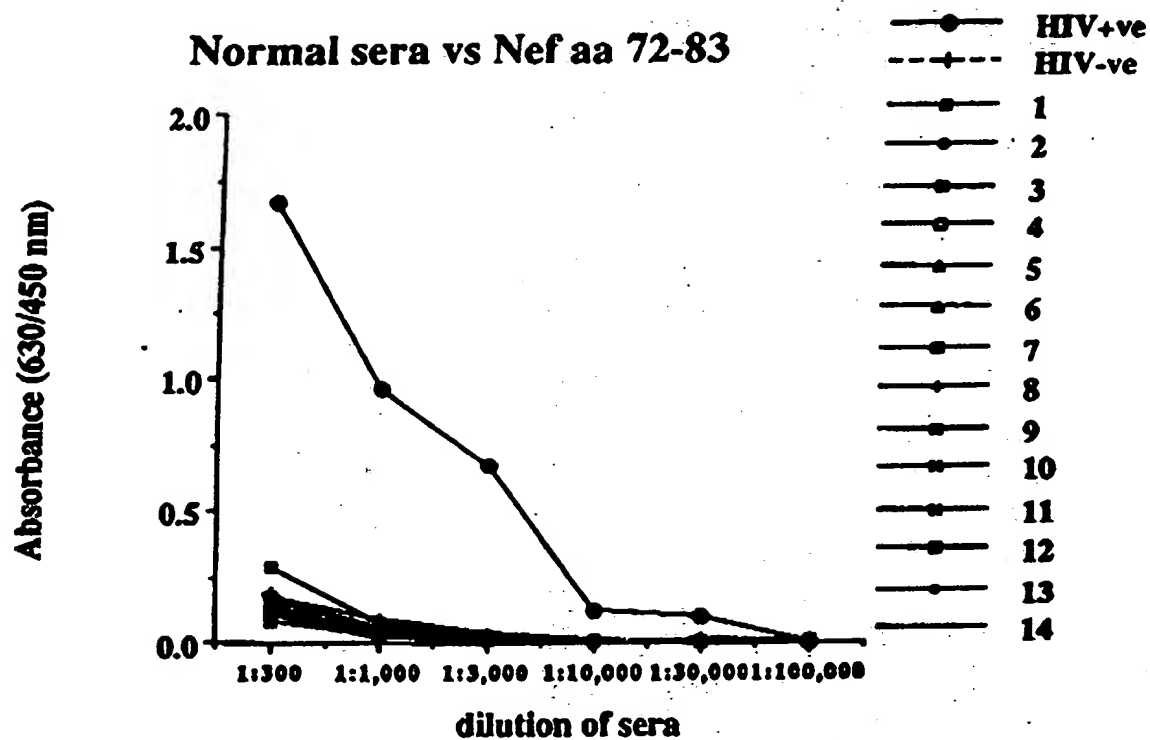


FIGURE 13B (i) (iv)



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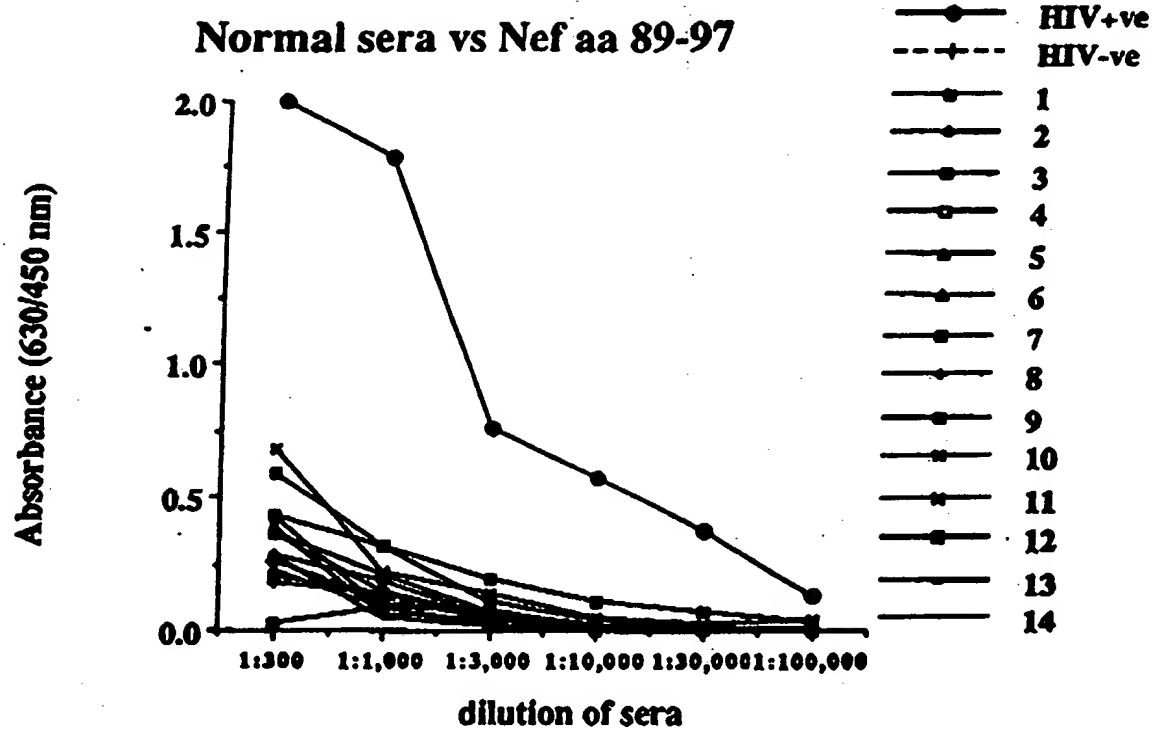
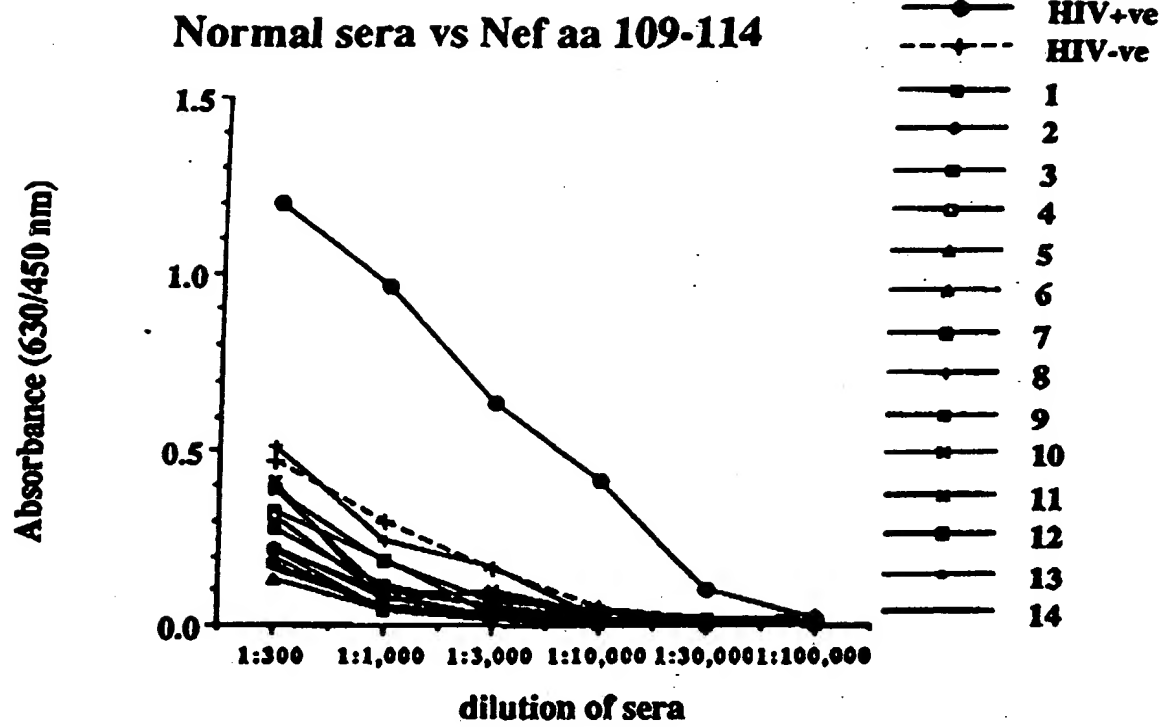
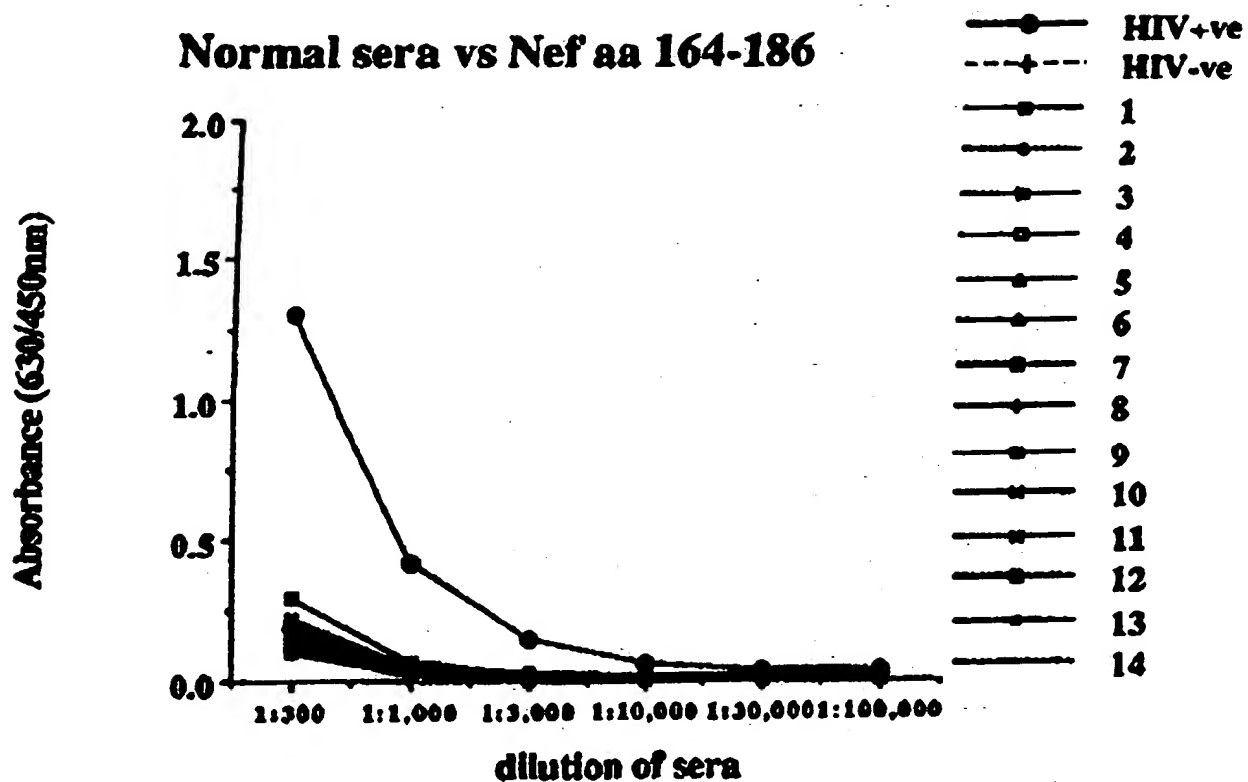


FIGURE 13B (i) (vi) 67/101



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FIGURE 13 B (i) (vii)



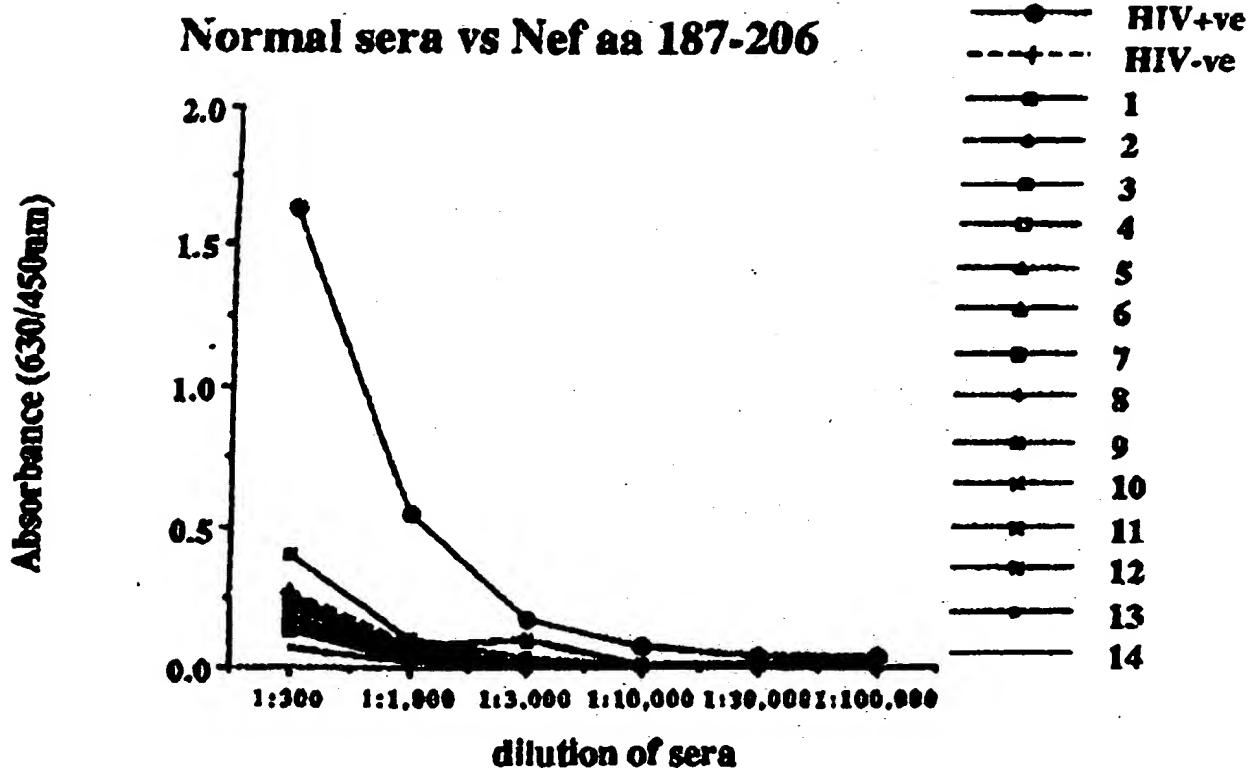
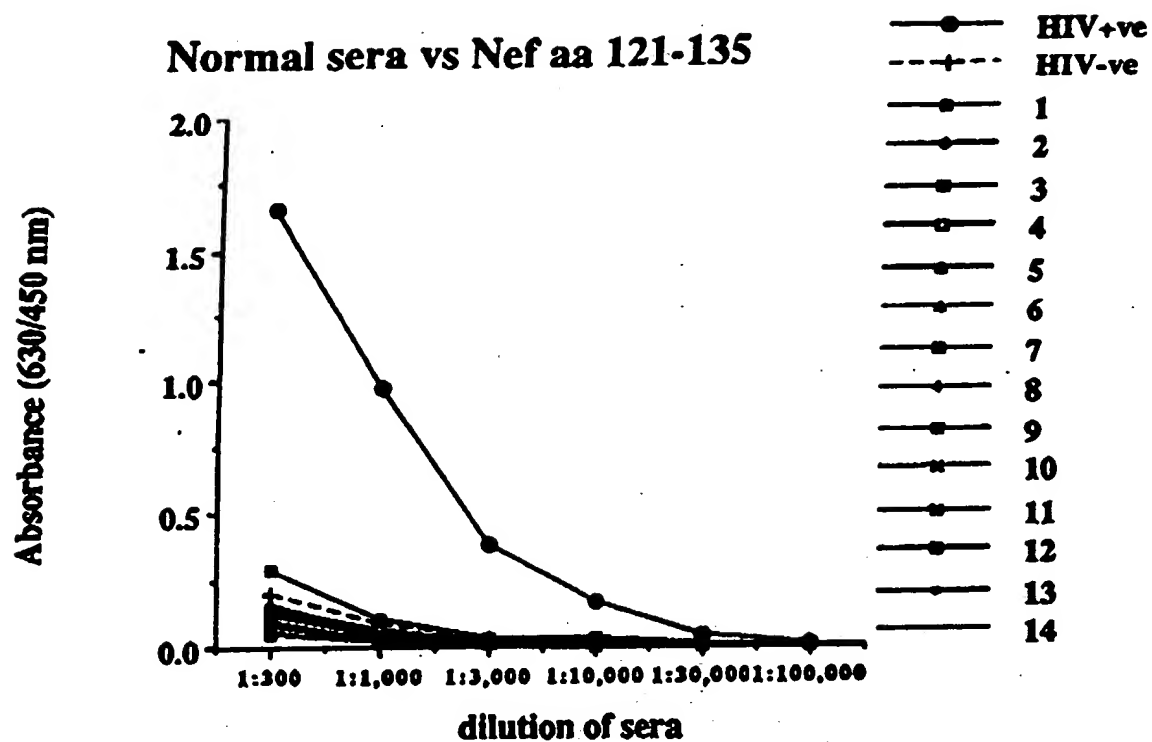


FIGURE 13B (i) (ix) ^{70/101}



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FIGURE 13 B (i) (x)

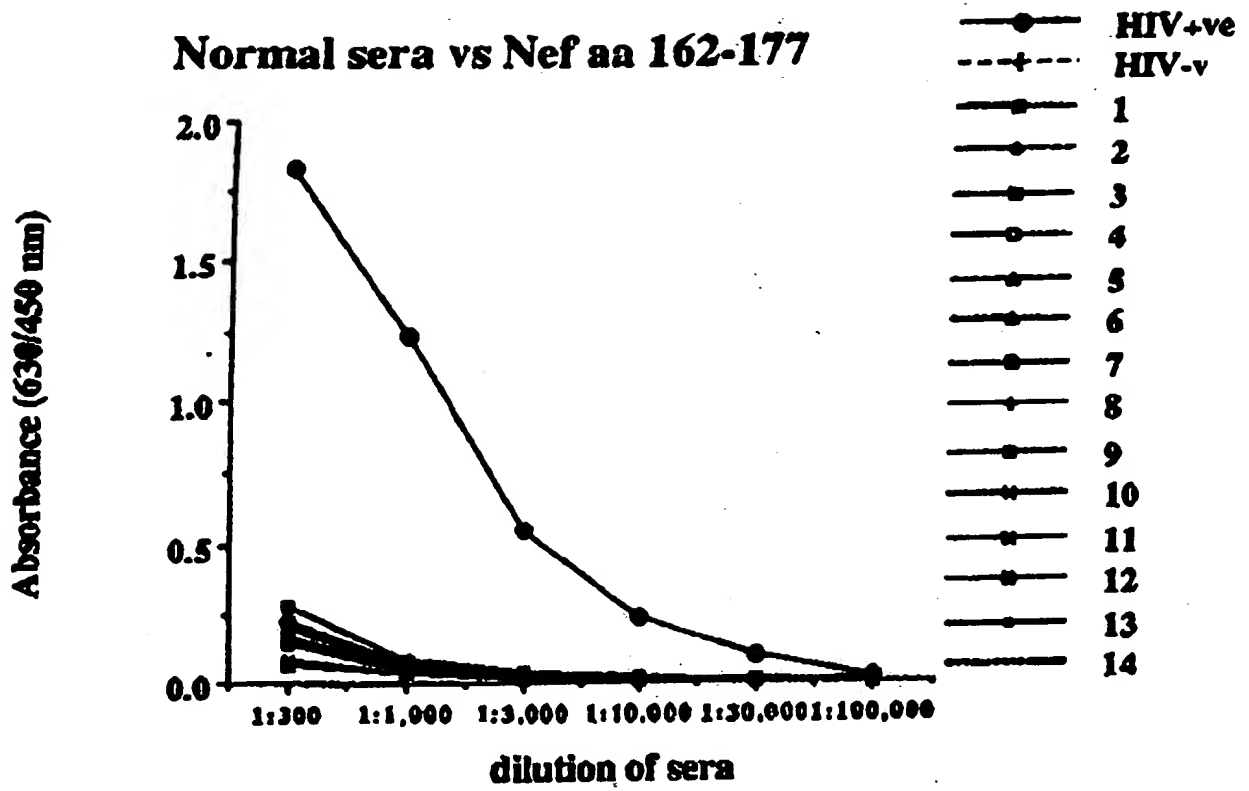


FIGURE 18 B (ii) (i) ^{72/101}

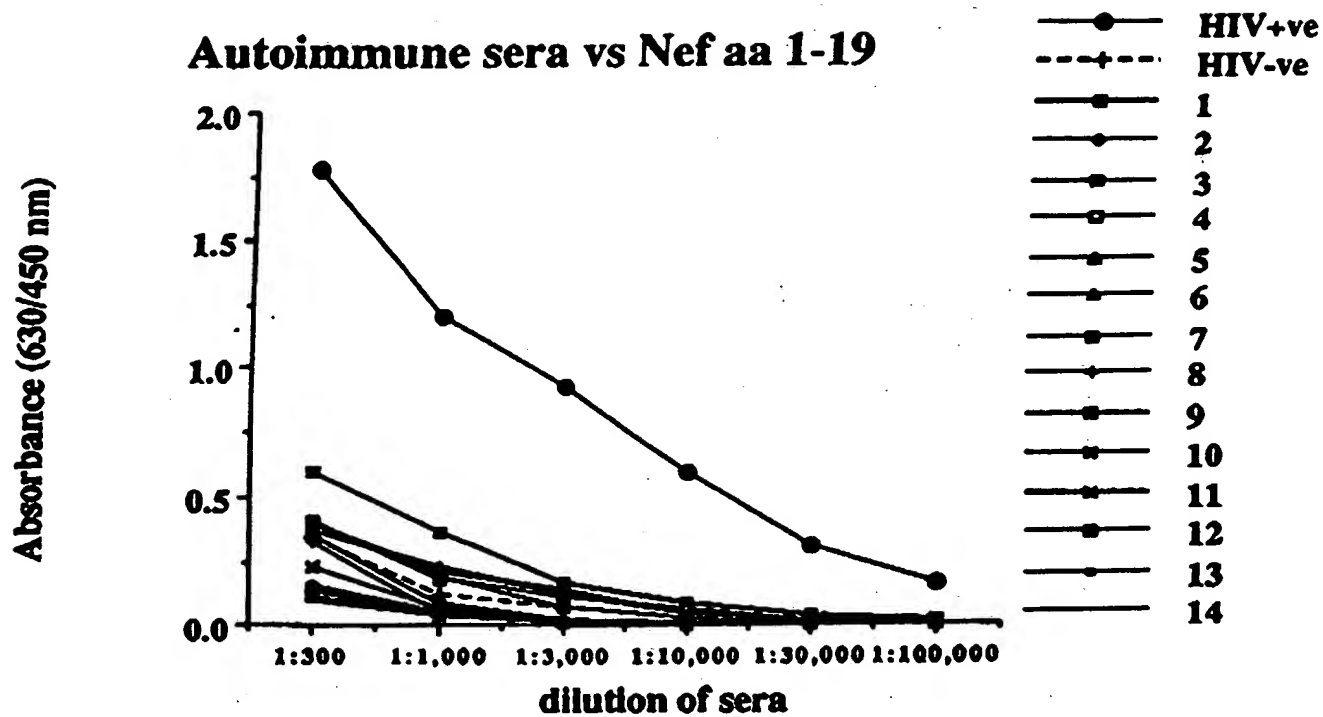
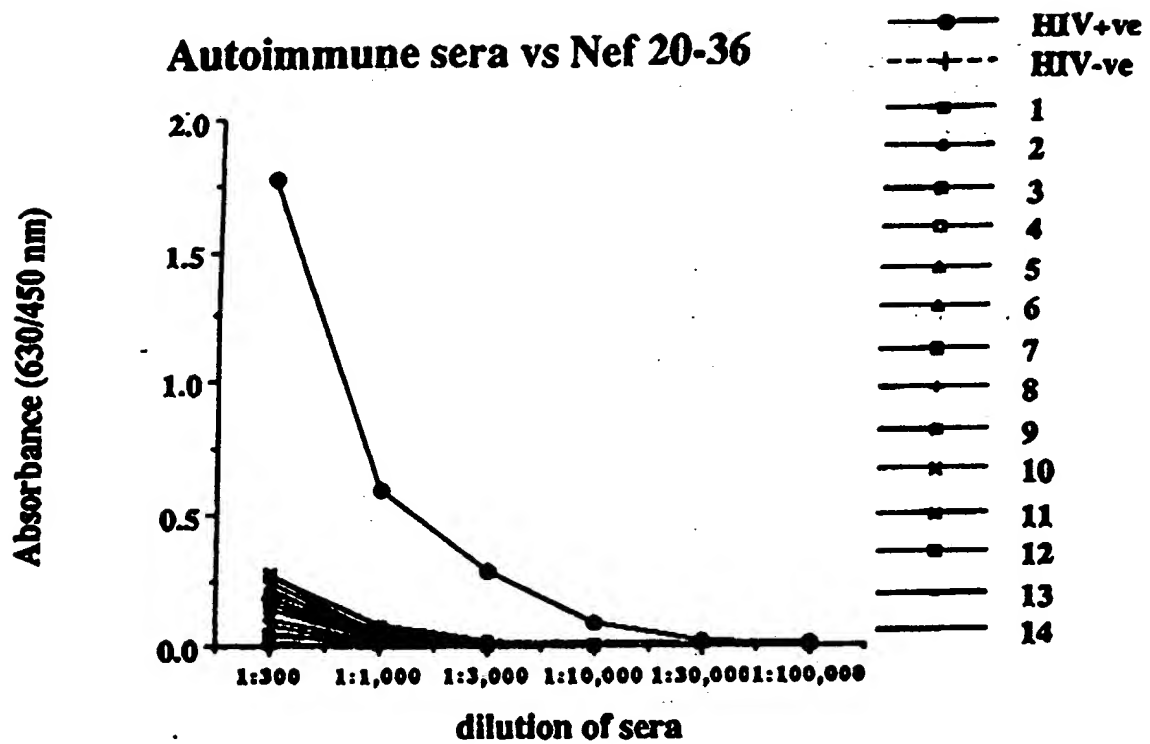
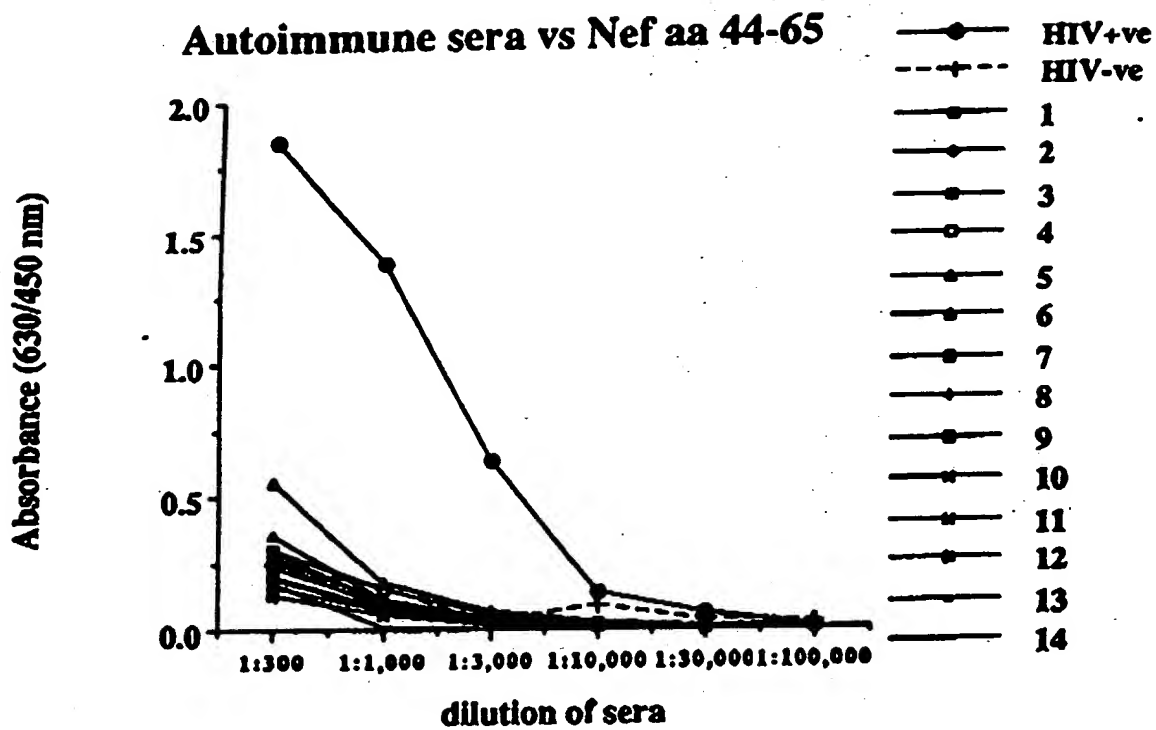


FIGURE 13 B (ii) (i) ^{73/101}



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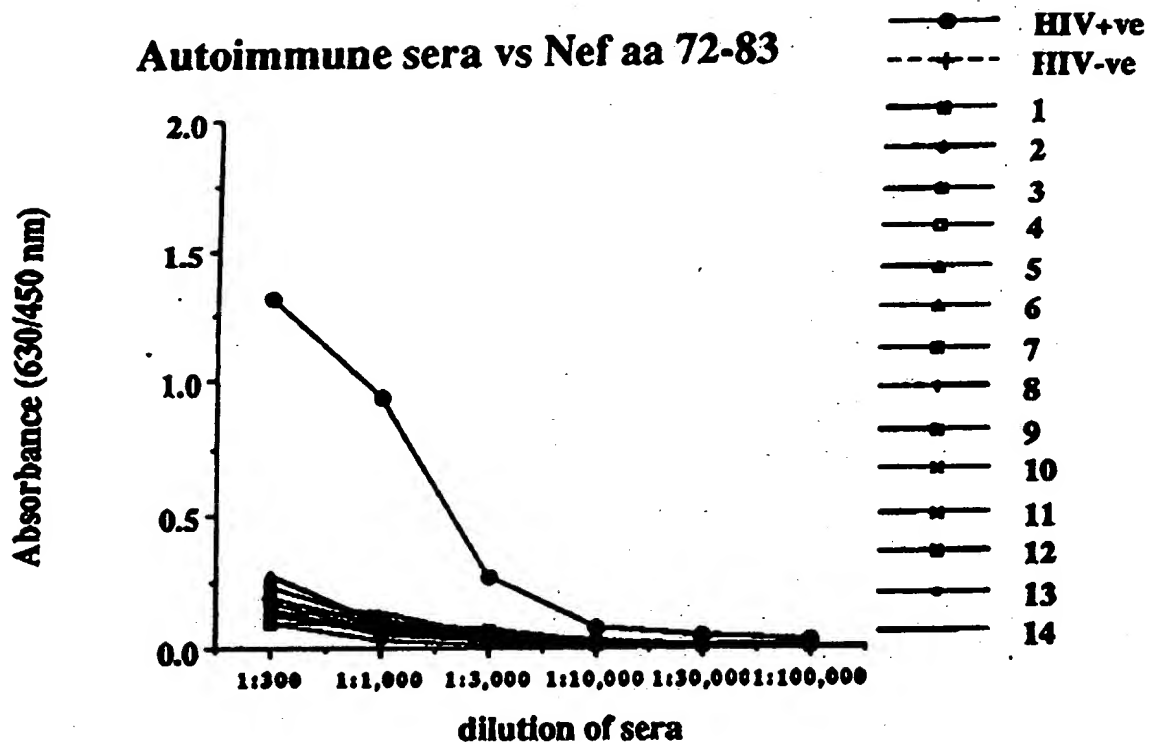
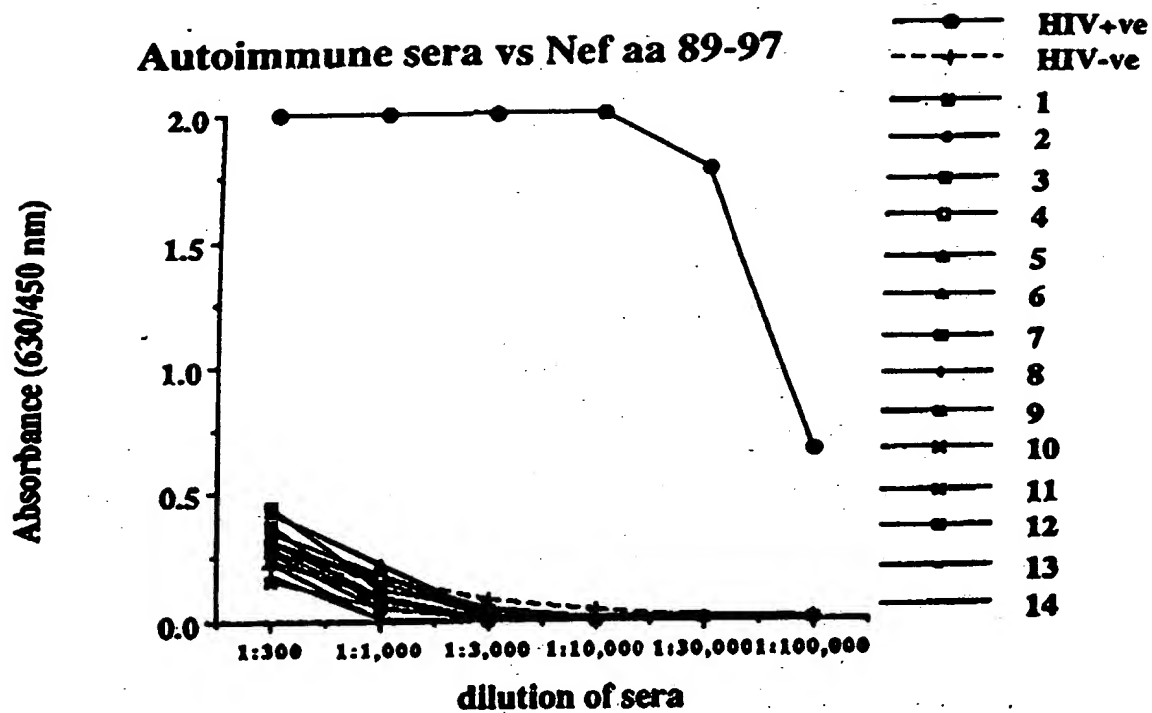
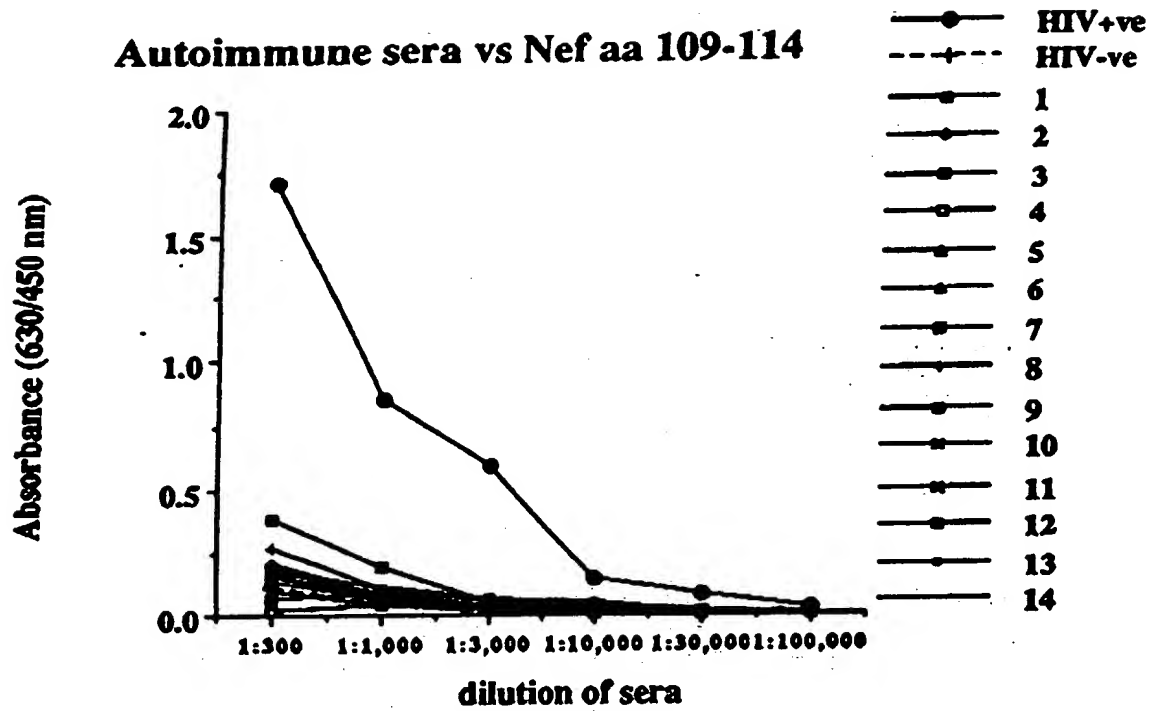


FIGURE 13B(ii) (v)

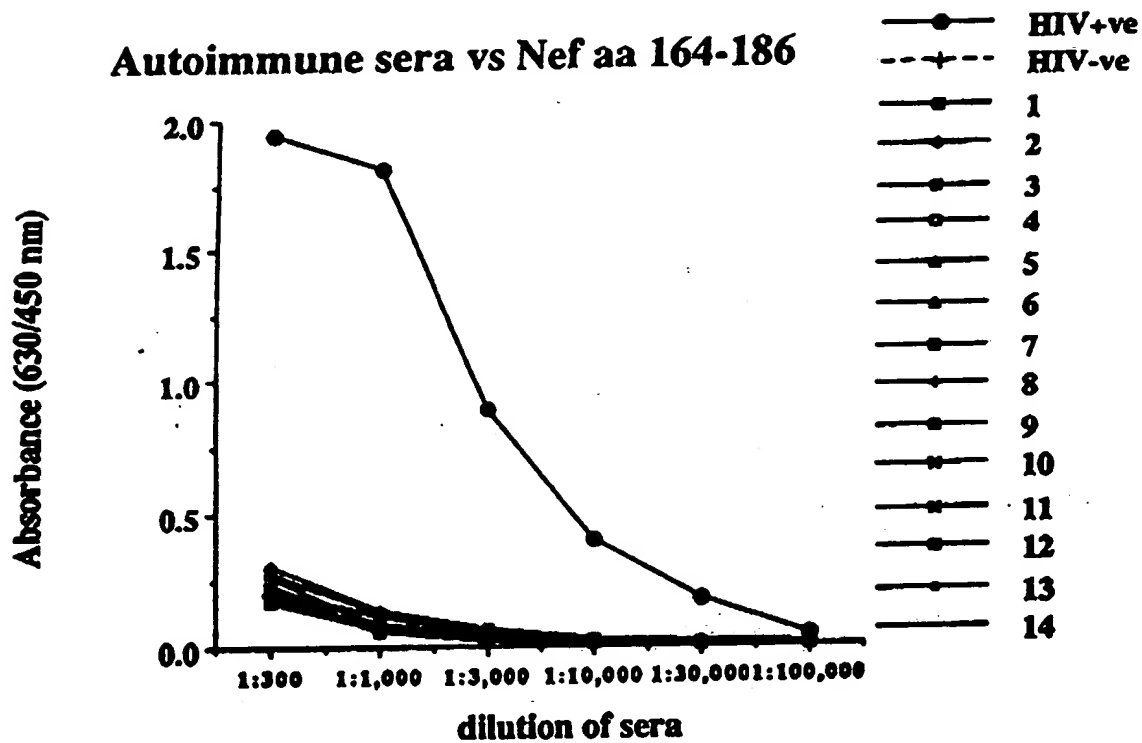


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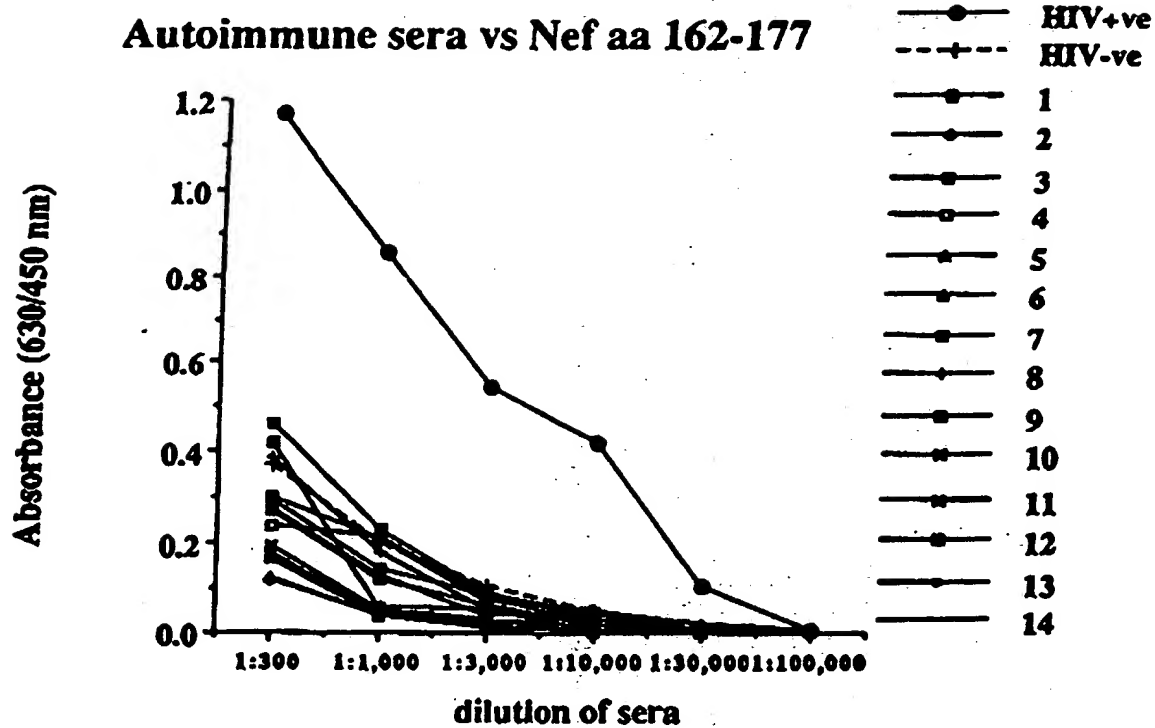


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FIGURE 13 B (ii) (vii)

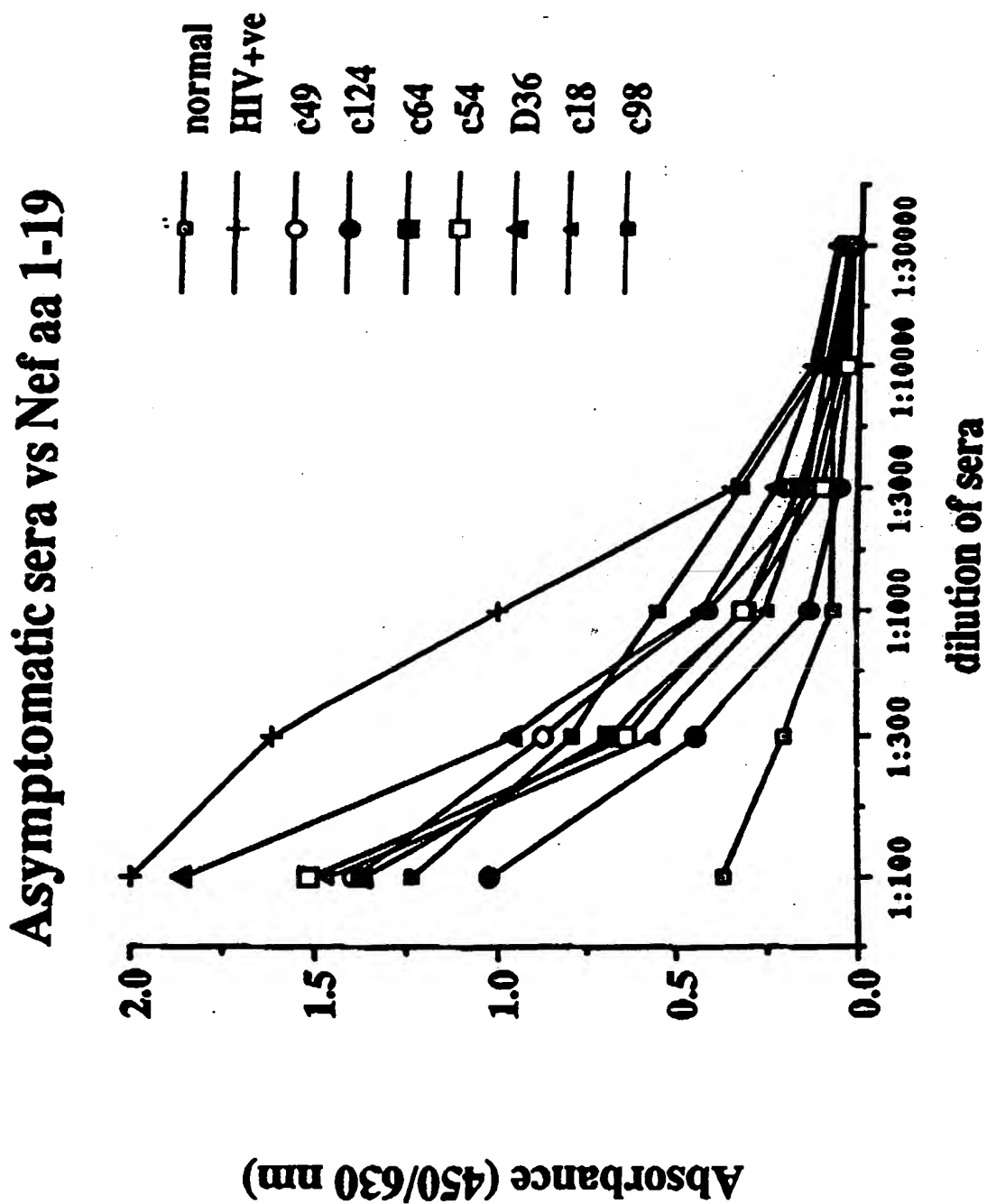


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FIGURE 13 B (11) (x)

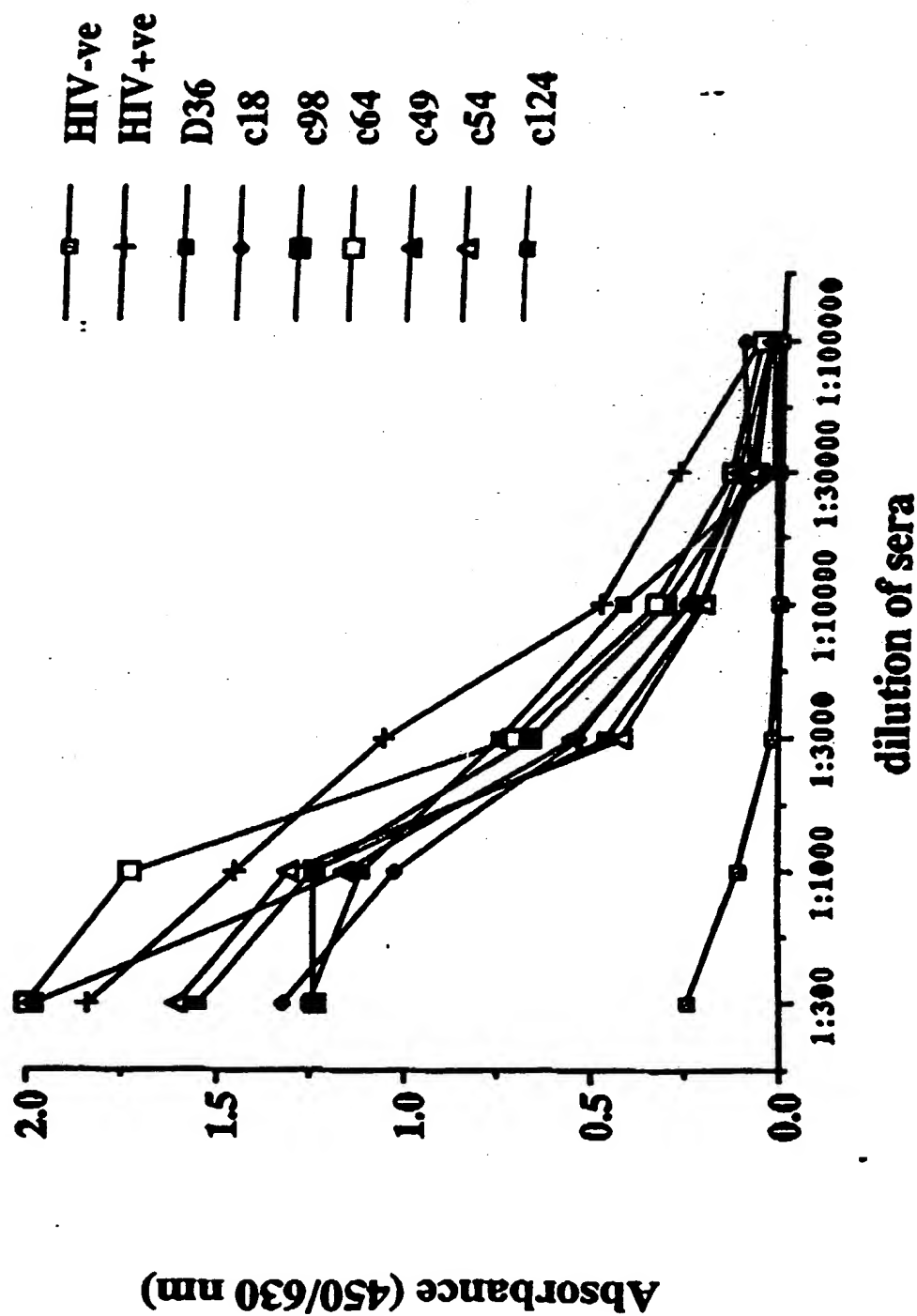


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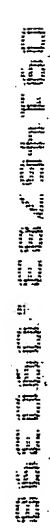
FIGURE 13C (i)



Asymptomatic sera vs Nef aa20-36

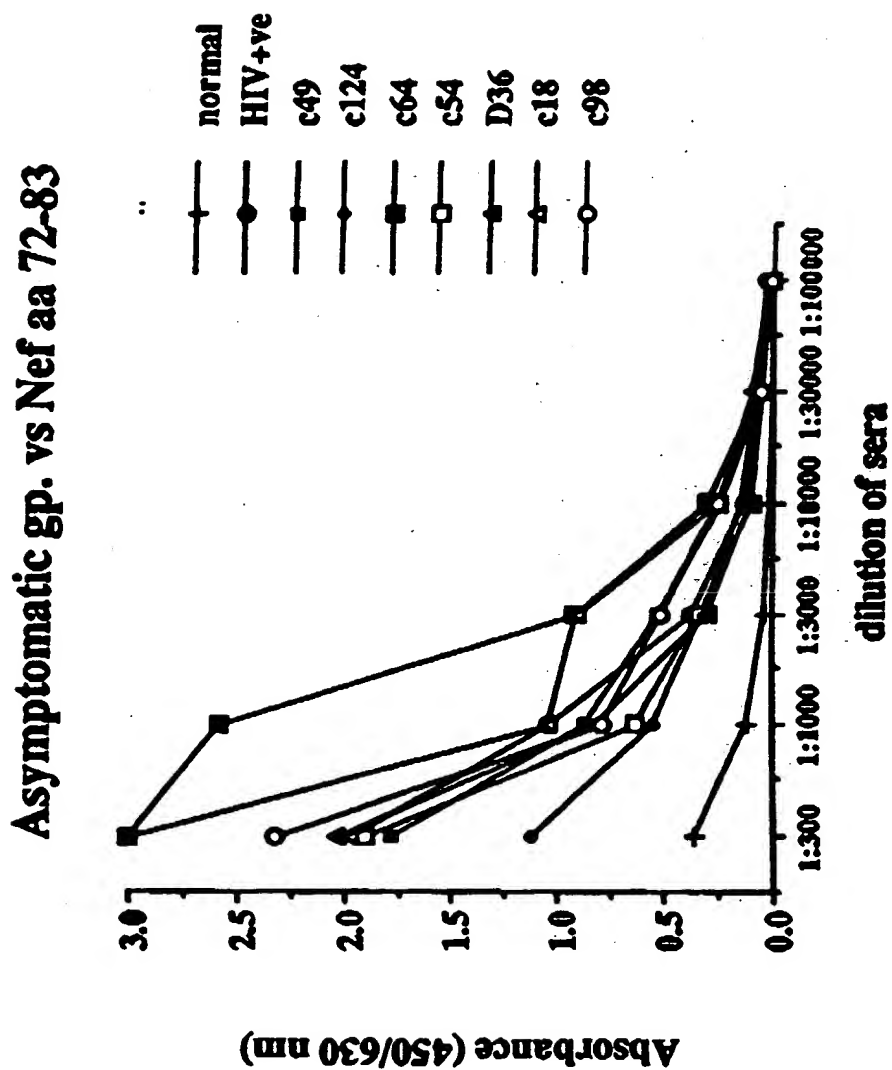


.



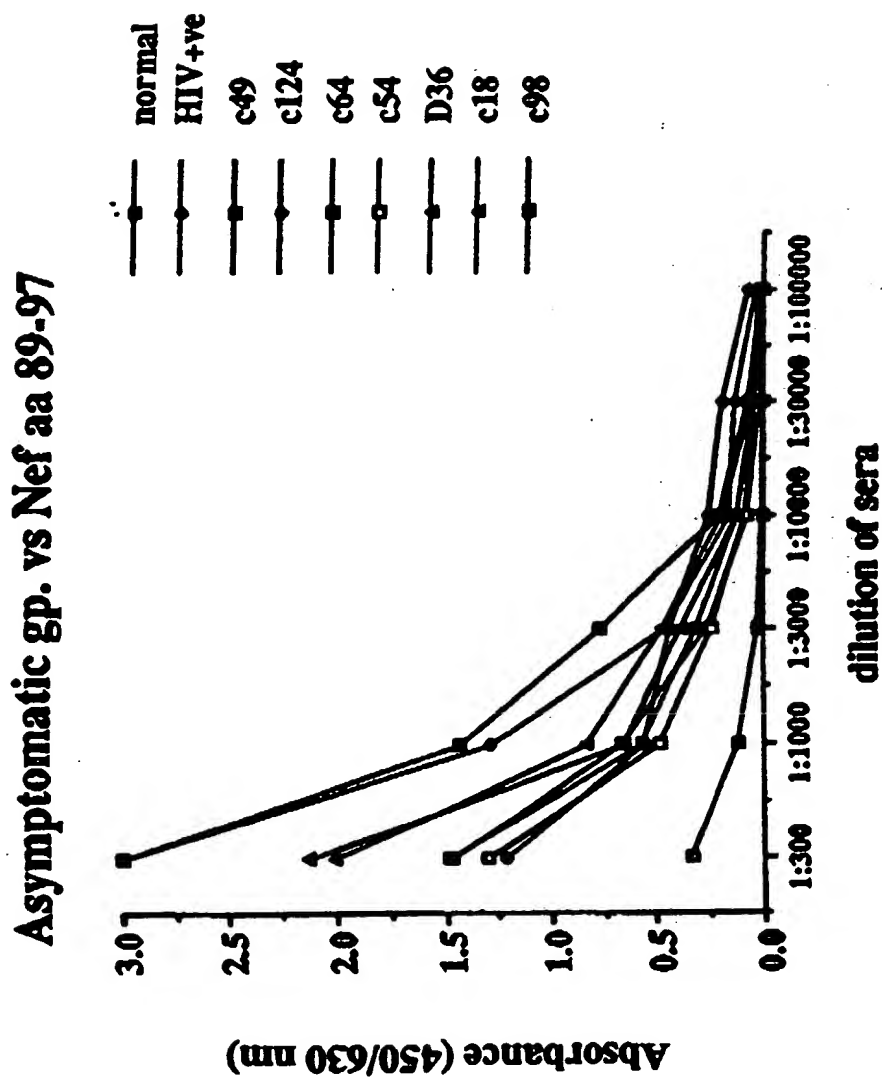
Asymptomatic gp vs Nef 44-65

FIGURE 13C (iv)



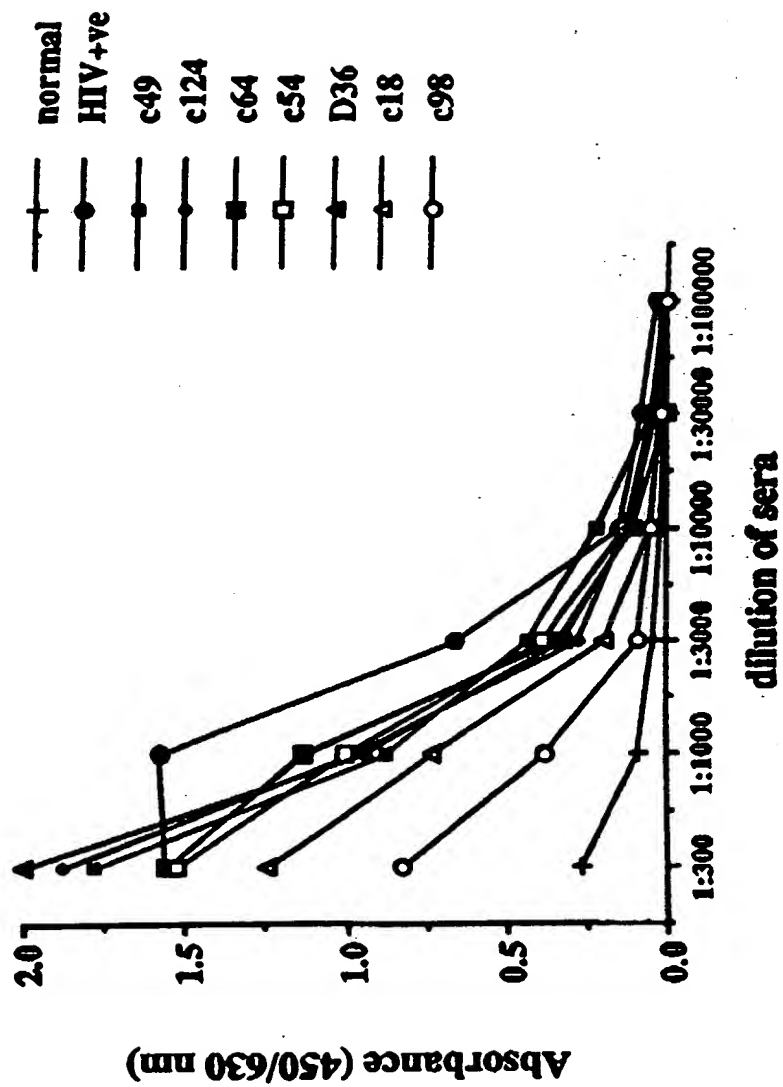
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FIGURE 13C (v)



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Asymptomatic gp. vs Nef aa 109-114



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FIGURE 13C (vii)

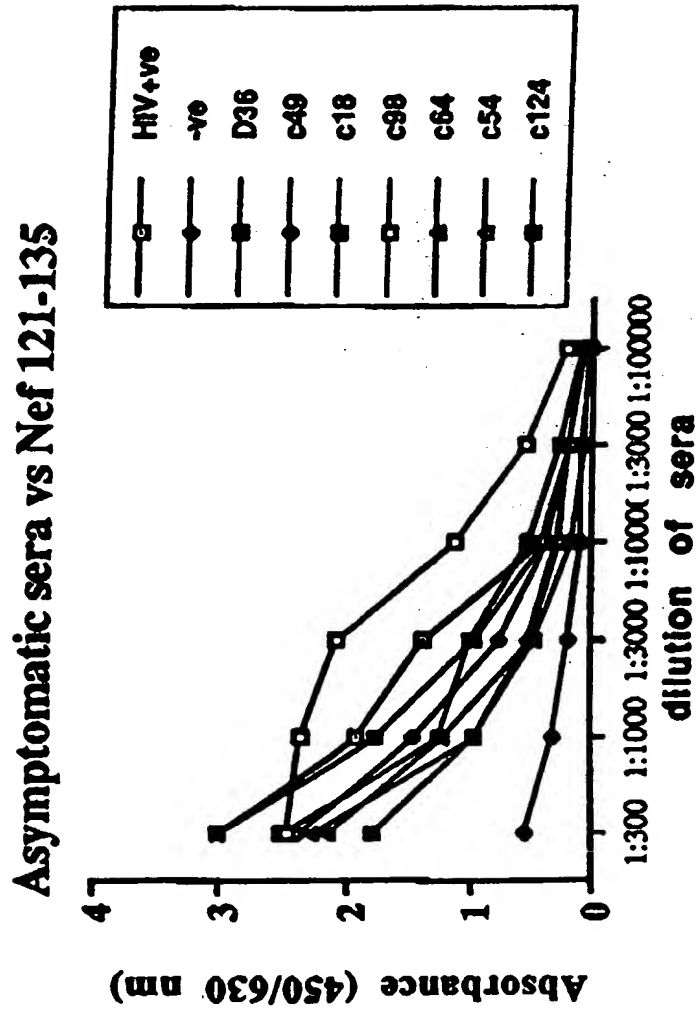


FIGURE 13C (viii)

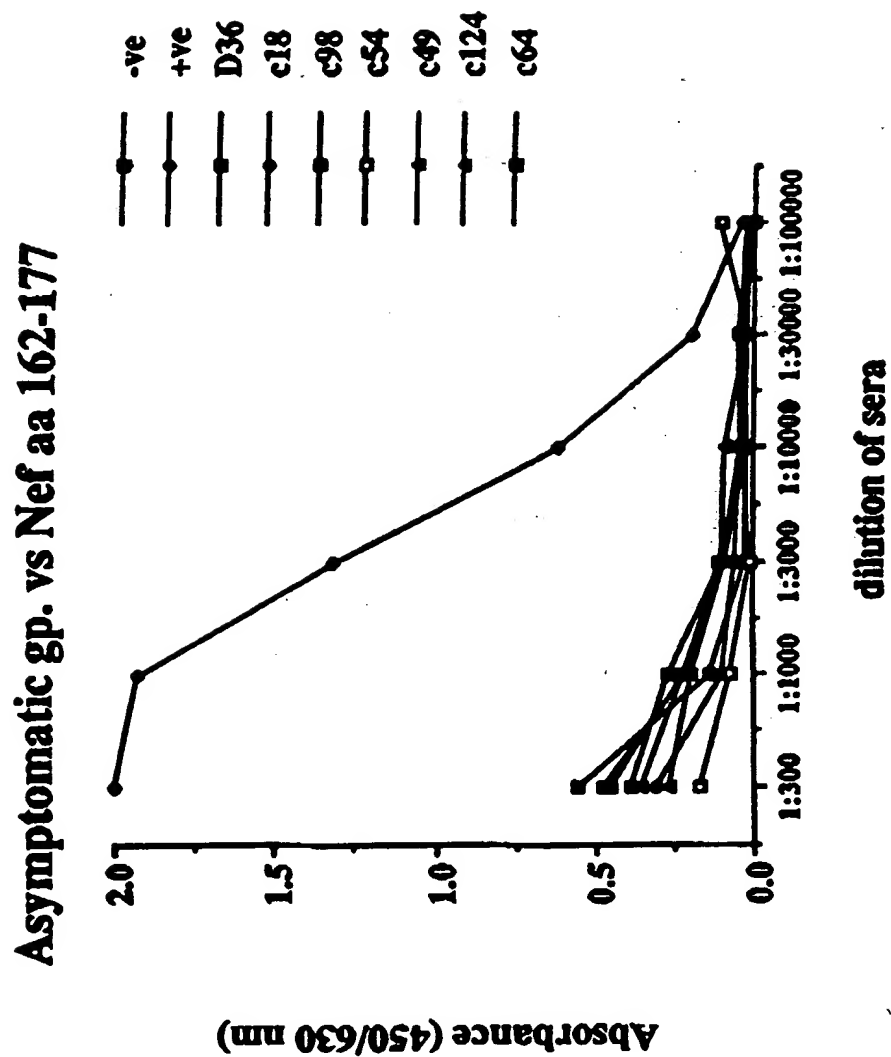


FIGURE 13C (ix)

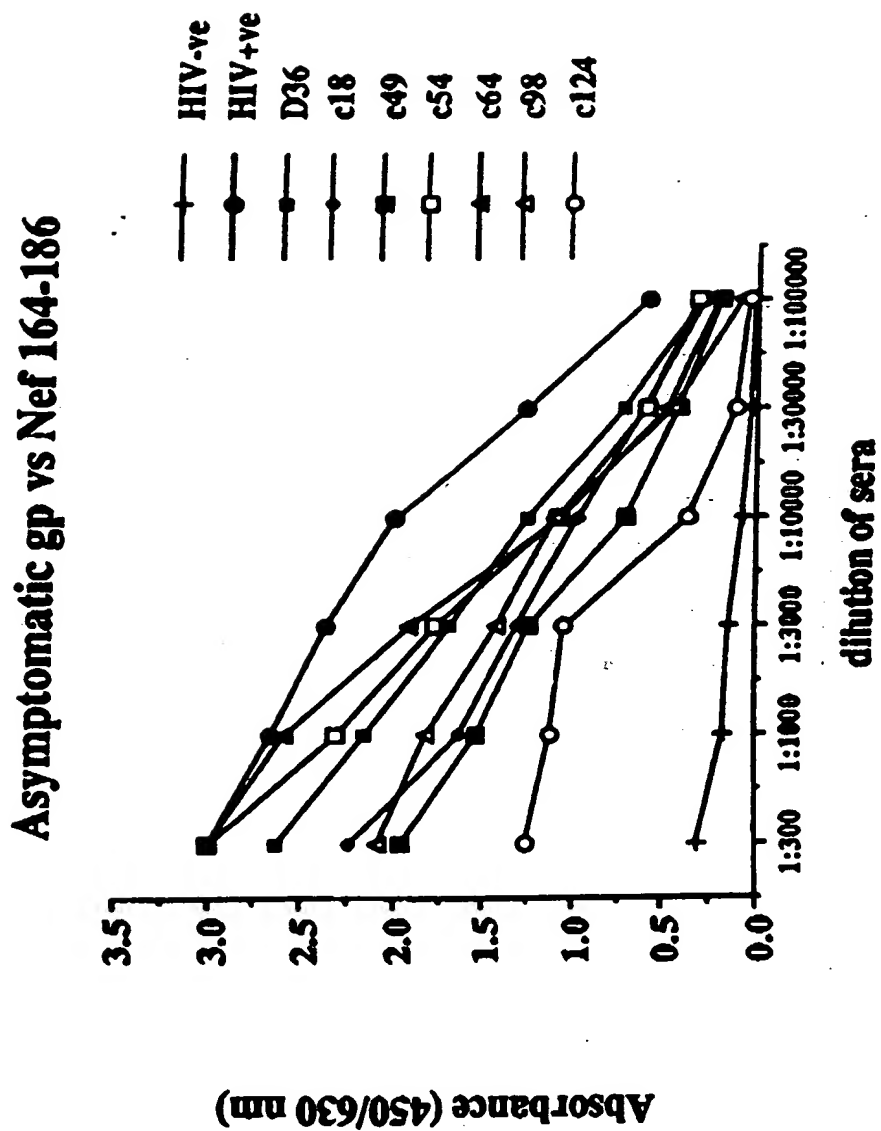
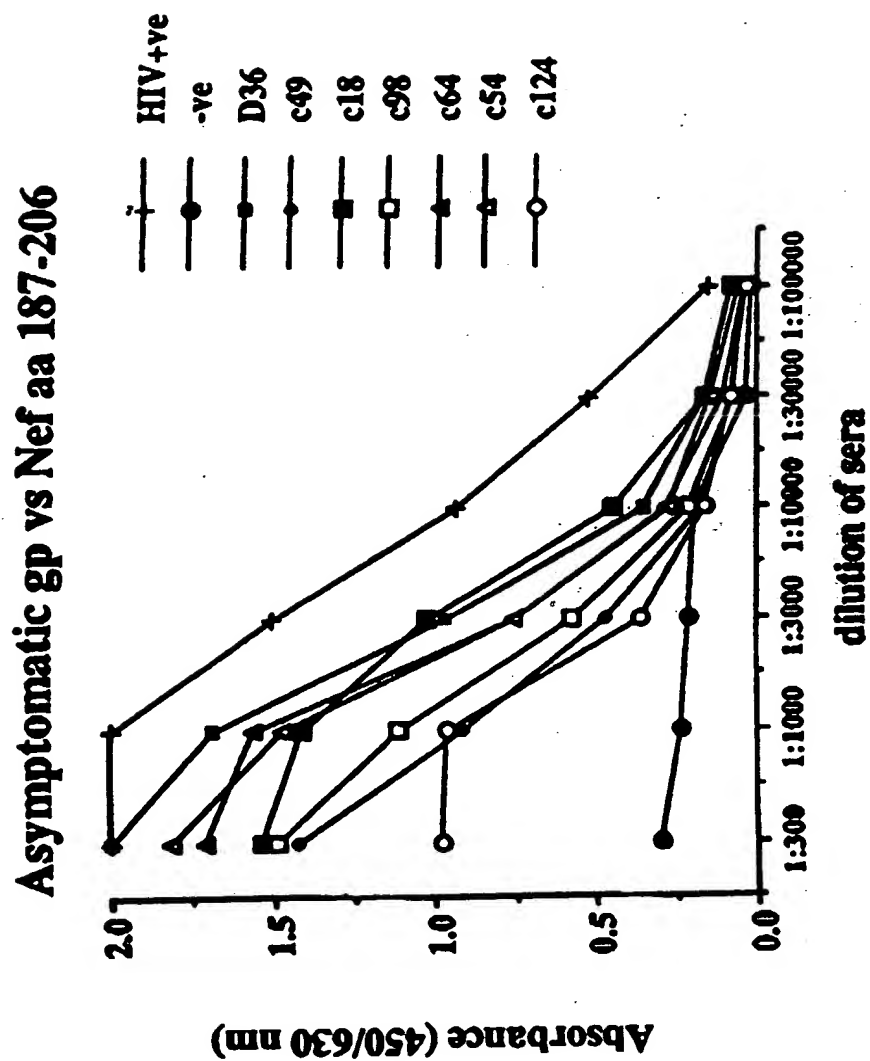
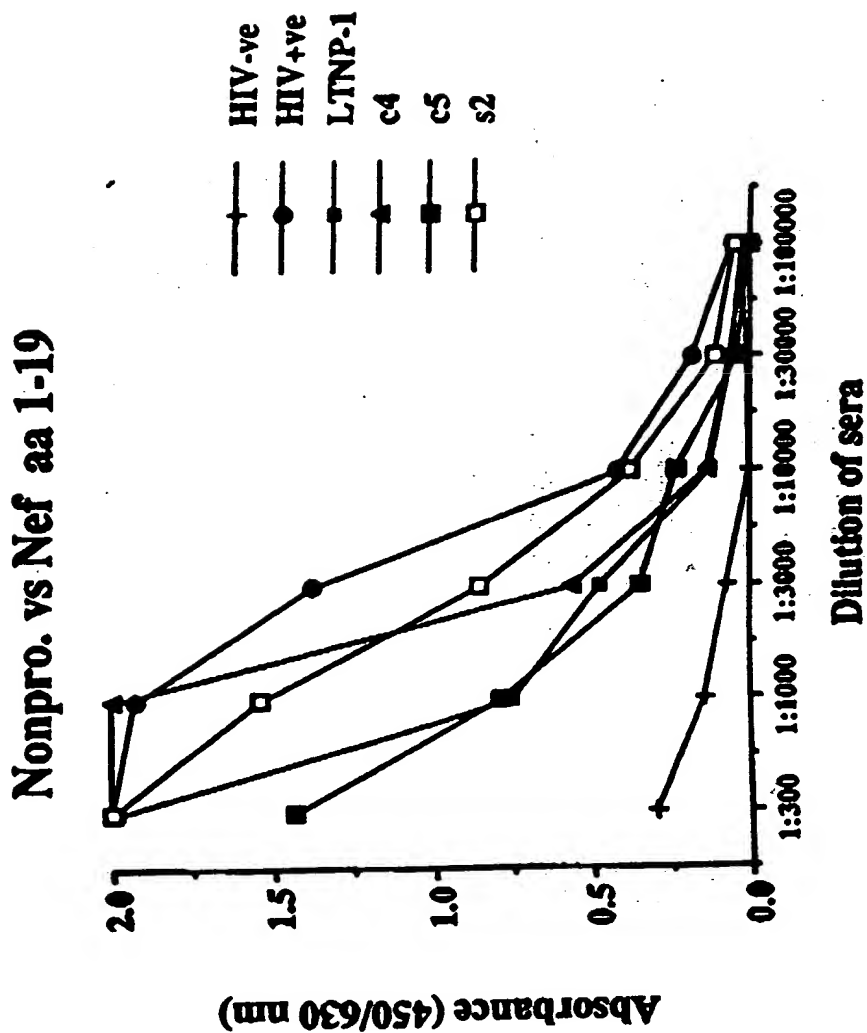


FIGURE 13C (x)



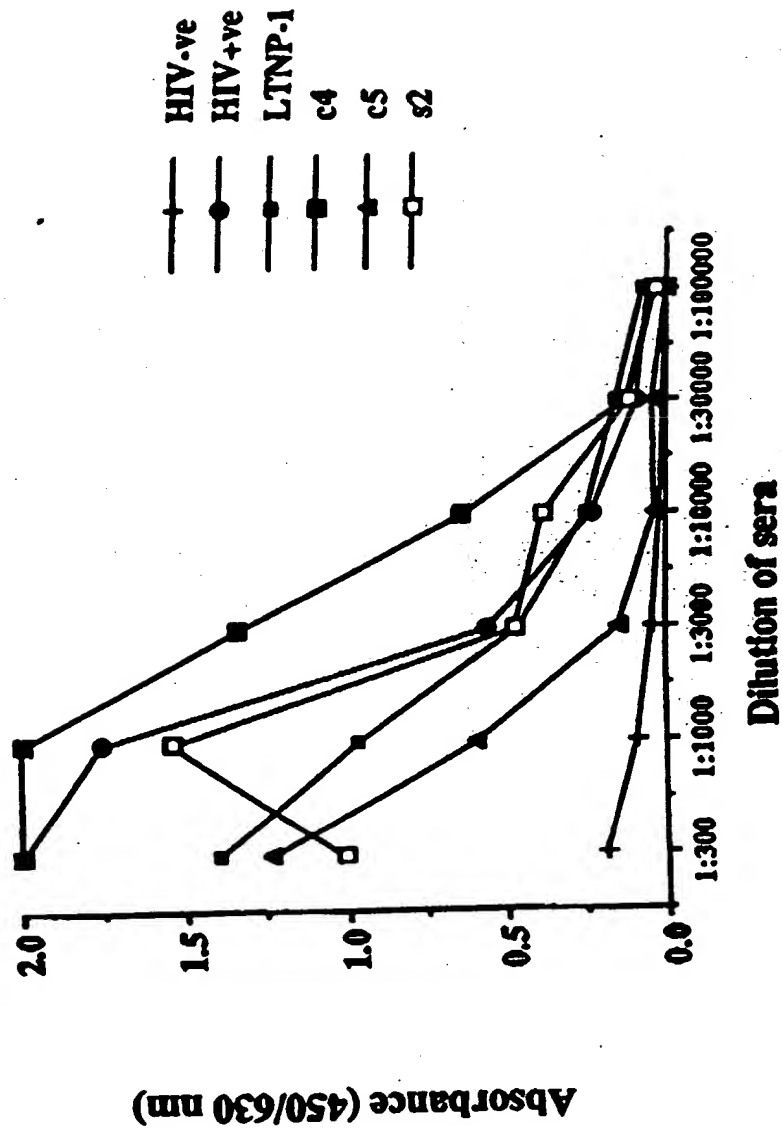
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FIGURE 13D (i)



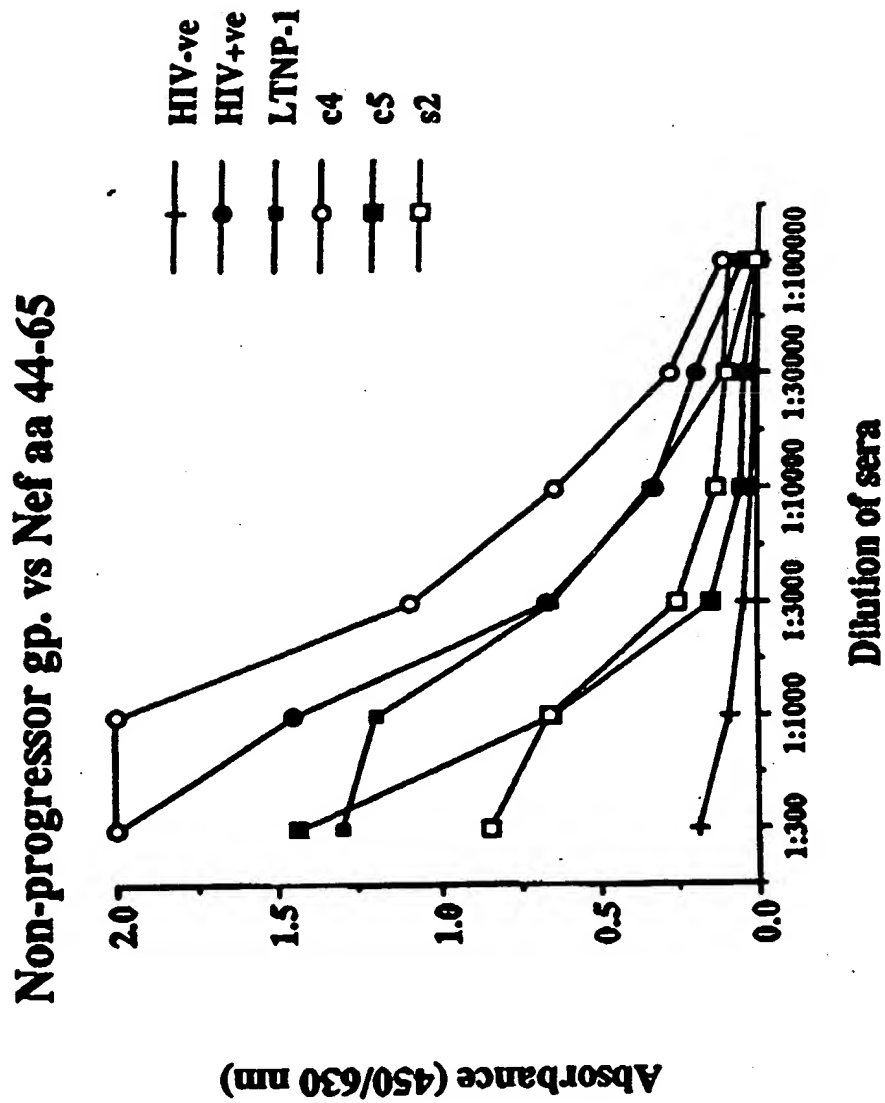
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FIGURE 13D (ii)

Non-progressor. vs Nef aa 20-36



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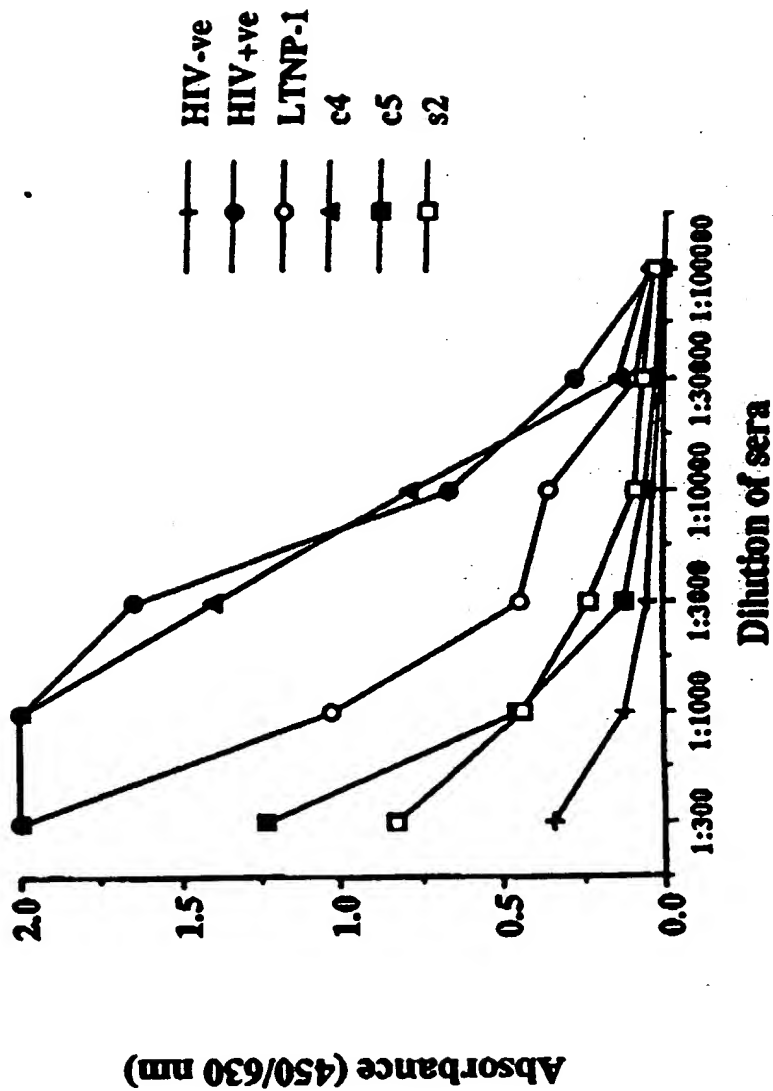
FIGURE 13D (iii)



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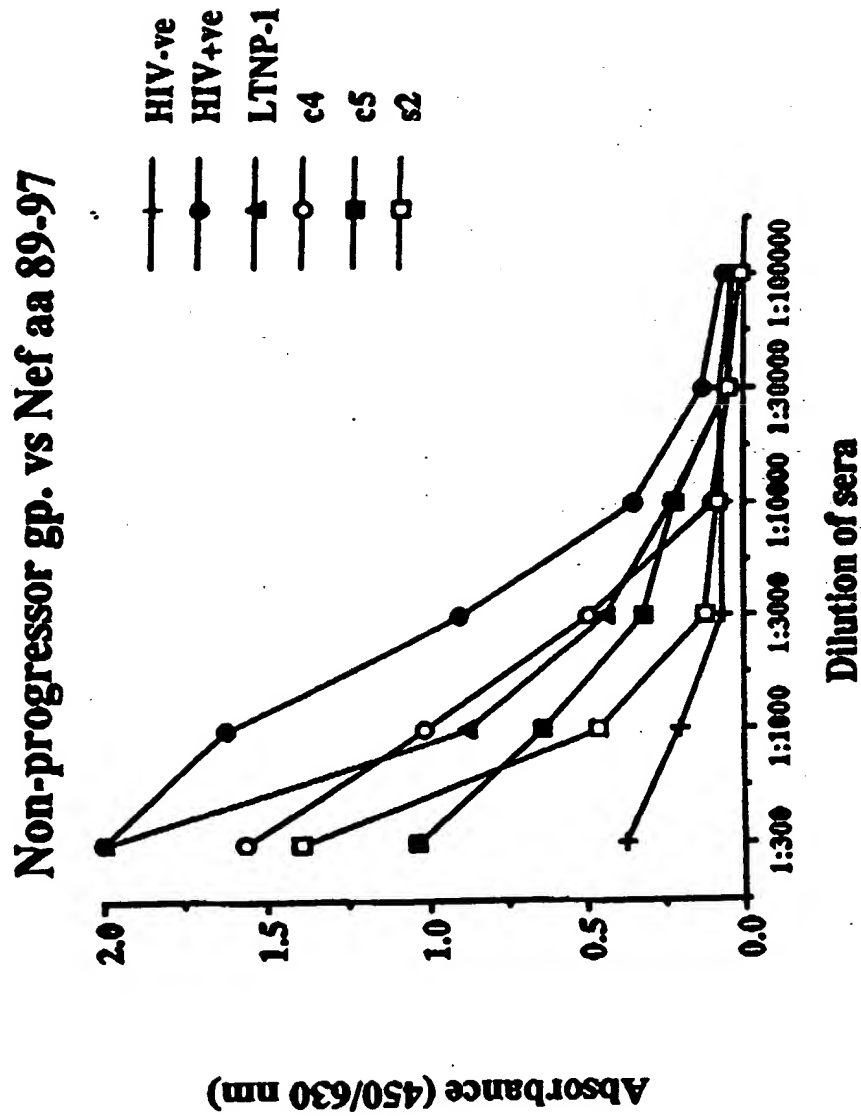
FIGURE 13D (iv)

Non-progressor gp. vs Nef aa 72-83



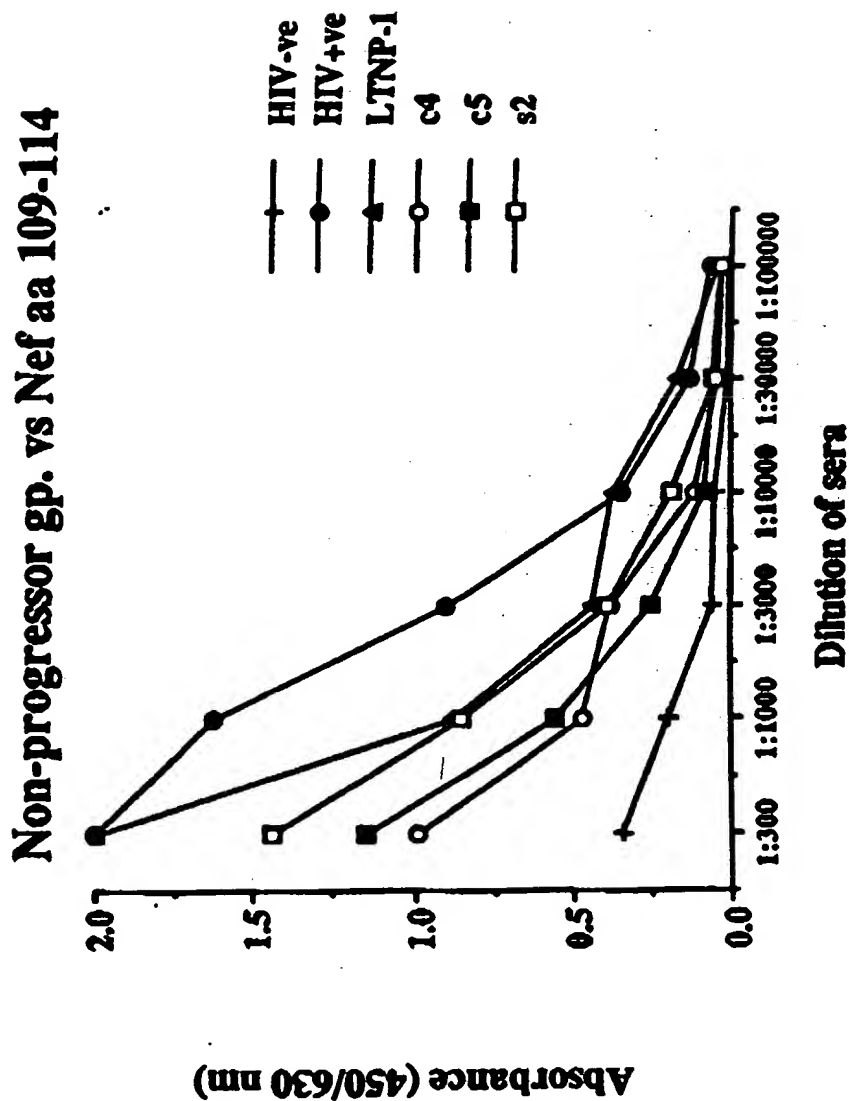
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FIGURE 13D (N)



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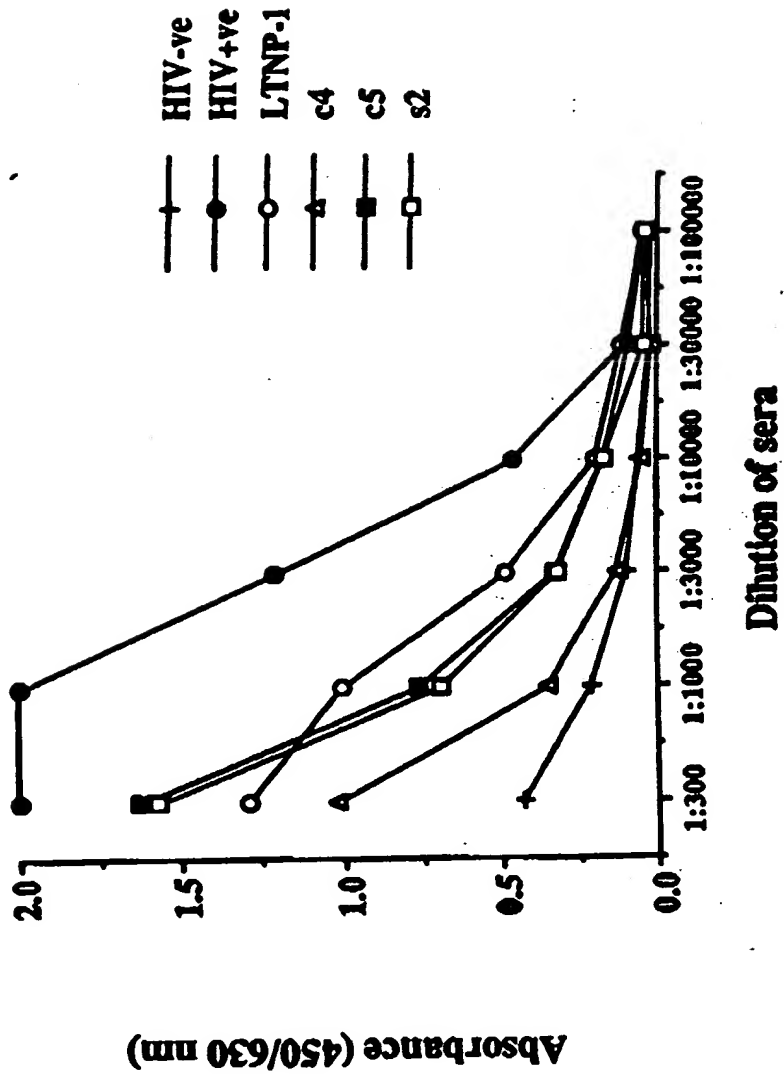
FIGURE 13D (vi)



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FIGURE 13D (viii)

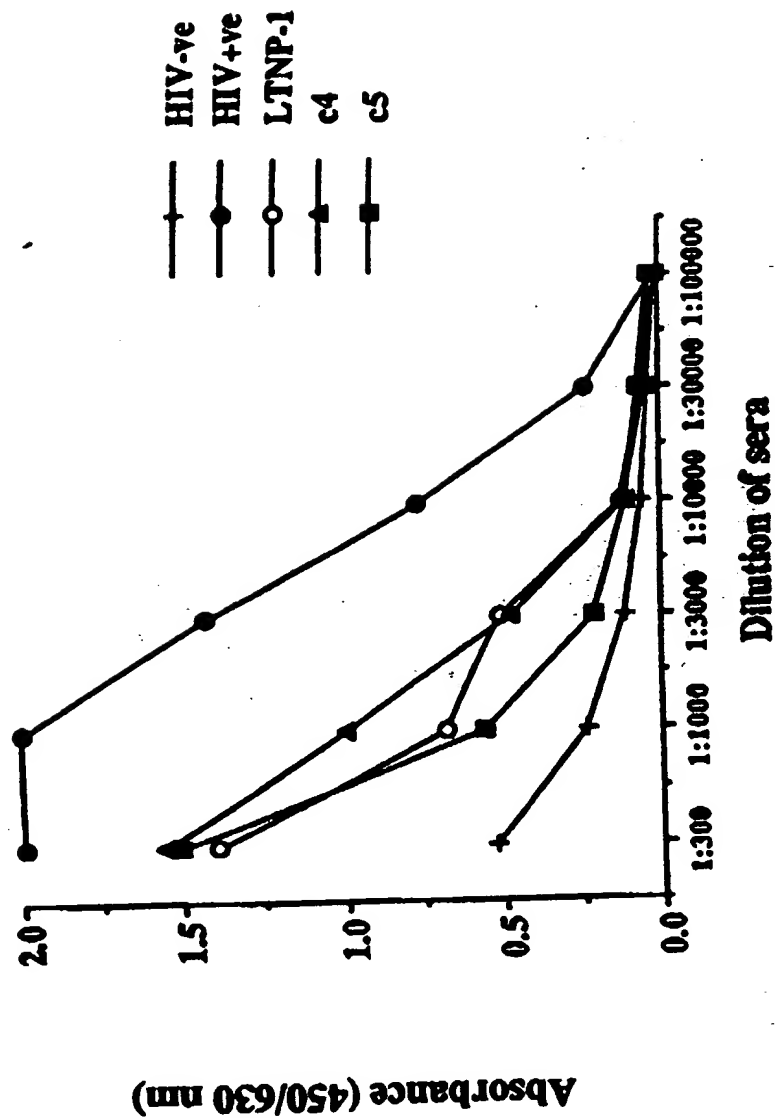
Non-progressor gp. vs Nef aa 121-135



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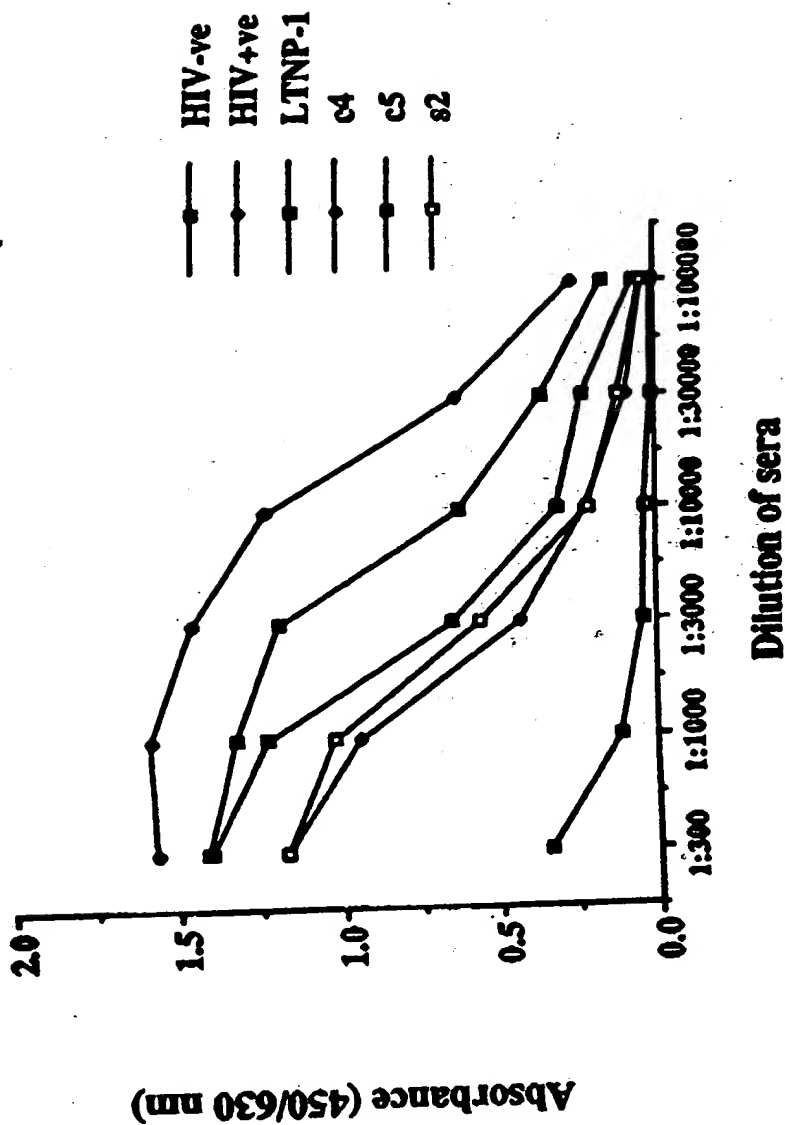
FIGURE 13D (viii)

Non-progressor gp. vs Nef aa 162-177



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FIGURE 13D (ix)

Non-progressor gp. vs Nef aa 164-186



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FIGURE 13D (x)

Non-progressor gp. vs Nef aa 187-206

